GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
A_Geneseq_032802:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-883-2
868
1 MKKALATLIALALPAAALAE.....VNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

MMUS

Result	Score	Query Match Length DB	ength	DB.	IJ	Description
1	868	100.0	174	17	AAW04891	Proteinase K resis
2	854	98.4	174	17	AAW04893	Proteinase K resis
ω	825	95.0	174	17	AAW04894	Proteinase K resis
4	824.5	95.0	175	17	AAW04892	Proteinase K resis
ຫ	785	90.4	155	22	AAB19895	Neisseria meningit
6	135	15.6	170	16	AAR73911	Neisseria meningit
7	133	15.3	25	17	AAW04912	N. meningitidis 60
8	94.5	10.9	212	22	AAU34556	E. coli cellular p
9	94	10.8	353	22	AAB47447	MOMP P5. Haemophi
10	89.5	10.3	257	22	AAU38252	Salmonella typhi c
11	88.5	10.2	180	21	AAY84612	The outer membrane

Fibronectin attach	TAZ/61WW	77	323	٧.٧	19.5	ũ
Actinobacillus ple	œ	2 2	215	9.2	79.5	4
Actinobacillus ple	AAY96096	21	215	•	9	ù
Blood group antige	AAW41523	19	707	•	· &	N
Arabidopsis thalia	AAG32501	21	511	•	80	Ë
	AAG09861	21	511	•	80	0
	AAW21678	18	390	•	80	Ö
Arabidopsis thalia	AAG52874	21	316	9.2	80	æ
Attachment-invasio	AAR96207	17	162	•	80.5	7
$^{\circ}$	AAG92581	22	261	•	81	ō
N. meningitidis 60	AAW04909	17	15	•	81	ເົາ
M. catarrhalis str	AAY43382	20	512	9.4	82	4
Arabidopsis chloro	AAW41732	19	433	9.4	82	ũ
Chlamydia trachoma	AAY36955	20	797	9.5	82.5	Ñ
H. pylori outer me	AAY17210	20	704	•	82.5	ï
Actinobacillus ple	AAY97899	21	364	•	83	ö
Actinobacillus ple	AAY96097		364	9.6	83	õ
Virulence gene pro	AAB44588		364	•	83	æ
Protein associated	AAB59179		350	9.7	84	7
Outer membrane pro	AAP82053		350	•	84	õ
•	AAR96210		568	9.8	. 85	ίň
Arabidopsis thalia	AAG09860	21	534	•		4
Arabidopsis thalia	AAG52873	21	339	•	85.5	ū
Non-typable Haemop	AAR66294	16	359	9.9	86	ผ
Cysteine protease	AAB65766	22	500		87	μ
N. meningitidis 60	AAW04901	17	16	10.0	87	ö
H. pylori bacteria	AAY78360	21	708	10.1	87.5	عا
Helicobacter pylor	AAW73022	19	708	10.1	7	œ
M. catarrhalis str	AAW68208	19	889	10.1	88	7
	AAW68204	19	624	10.1	88	Ġ
catarrhalis	AAW68206	19	610	10.1	88	Ü
rn	AAW68202	19	573	٠	8	4
gin	AAY34400	20	221	10.2	88.5	w
Porphorymonas ging	AAY34533	20	204	10.2	œ	N

ALIGNMENTS

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RESULT 1
AAW04891
ID AAW0
XX
Key
Peptide
       Brodeur BR,
                                         04-AUG-1995;
17-MAR-1995;
                                                                                                                               Protein
                                                                                                                                                                                          Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                         AAW04891;
                                                                                                                                                                                                                                                                          AAW04891 standard;
                        (IAFB-) IAF BIO VAC INC
                                                                                     26-SEP-1996
                                                                                                                                                                          Neisseria
                                                                                                                                                                                                                     Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                       22-DEC-1996
                                                                   15-MAR-1996;
                                                                                                     WO9629412-A1.
                                                                                                                                                                          meningitidis strain 608B.
                                                                                                                                                                                                                                       (first entry)
       Hamel J, Martin D,
                                        95US-0001983.
95US-0406362.
                                                                   96WO-CA00157.
                                                                                                                               /label= sig_peptide 20..174
                                                                                                                                                        Location/Qualifiers
                                                                                                                     /label= mat_protein
                                                                                                                                                                                                                                                                          Protein; 174 AA.
       Rioux C;
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RESULT 2
AAW04893
Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                           04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AANT39039 to AANT39042). The iso 22 kD antigen, antigenic fragments of antibhodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection
           Brodeur BR,
                                                                                                   15-MAR-1996;
                                                                                                                                                    W09629412-A1
                                                                                                                                                                                         Protein
                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 1; 117pp; English.
                                  (IAFB-)
                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                      Neisseria meningitidis strain Z4063
                                                                                                                                                                                                                                                                                                                  Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                    AAW04893;
                                                                                                                                                                                                                                                                                                                                                                                             AAW04893 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         may also be used to detect antibodies specific to N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-443187/44.
N-PSDB; AAT39039.
                                                                                                                                                                                                                                                                               Neisseria
                                                                                                                                                                                                                                                                                                                                            22-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                   IAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                             gonorrhoeae;
                                                                                                                                                                                                                                                                                          K reistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 AA;
                                  BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
          Hamel J,
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                           95US-0001983
95US-0406362
                                                                                                  96WO-CA00157
                                                                                                                                                                                      /label= sig_peptide 20..174
                                                                                                                                                                          /label= mat_protein
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                             Neisseria meningitidis;
antibody; detection; pr
           Martin
                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 868; DB 17;
Pred. No. 4.1e-87;
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          Rioux
          Ç
                                                                                                                                                                                                                                                                             probe; surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 174;
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AAW04894
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AART3903) to AART39042). The isolated 4 strains of N. meningitidis of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis of by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis
           Brodeur
                                                              04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                         Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; pr
                                                                                                                                                                                                                                                                                                                                 Proteinase K resistant N. meningitidis
                                                                                                                                                                                                                                                                                                                                                             22-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                AAW04894 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Fig 9; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-443187/44.
N-PSDB; AAT39041.
                                  (IAFB-) IAF BIO VAC INC.
                                                                                                       15-MAR-1996;
                                                                                                                                  26-SEP-1996.
                                                                                                                                                           WO9629412-A1
                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                  Neisseria
                                                                                                                                                                                                                                                                                                                                                                                        AAW04894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequences encoding the antigen, or the as probes for the detection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Simhes 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
           BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                  meningitidis strain b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
           Hamel J,
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                             95US-0001983.
95US-0406362.
                                                                                                       96WO-CA00157
                                                                                                                                                                                                 /label= sig_peptide
20..174
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                                                                                                                                                                                     /label=
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           Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                 174
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Pred. No. 1.4e-85;
           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                          detection; probe;
           Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or their fragments,
                                                                                                                                                                                                                                                                                                                                   22 kD surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 174;
                                                                                                                                                                                                                                                                                          surface protein;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitidis or
                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be
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RESULT 4
AAW04892
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAW04892 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAR39039 to AAR39042). The isolated approximate the strains of antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                       Proteinase K resistant N. meningitidis 22 kD surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or diagnosis of, N. meningitidis infection
              Brodeur
                                                                  04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                     Neisseria meningitidis strain MCH88.
                                                                                                                                                                                                                                                                                              Proteinase K reistant; Neisseria meningitidis;
Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                                                                22-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-443187/44.
                                       (IAFB-) IAF BIO VAC INC.
                                                                                                          15-MAR-1996;
                                                                                                                                    26-SEP-1996.
                                                                                                                                                              WO9629412-A1
                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKALATLIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
            BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT39042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 10; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
            Hamel J,
                                                                95US-0001983.
95US-0406362.
                                                                                                         96WO-CA00157
                                                                                                                                                                                      /label= sig_peptide
20..175
/label= mat_protein
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%;
           Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 825; DB 17;
Pred. No. 2.1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenic Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
              Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunisation against,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 5
AAB19895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The iso 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis of by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 8; 117pp; English.
                                                                                                                                                                                                                                                            Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequences encoding the antigen, or their fragments, can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT39040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-443187/44
                       Region
                                                                                                                                               Region
                                                                                                                                                                                                Region
                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                     NspA; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                     19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                             AAB19895;
                                                                                                                                                                                                                                                                                                                                                                                    AAB19895 standard;
                                               Region
                                                                        Region
                                                                                                Region
                                                                                                                       Region
                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                           Neisseria meningitidis NspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKALAALIALAAAAAAAAAGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                                                                                                                                                                                            meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AA;
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the detection of pathogenic Neisseria
                                                                        /note=
63..74
/note=
78..88
                     /note= "s
                                                 /note=
89..104
                                                                                                                                               40..
/note= "t
                                                                                                                                                                       /note=
27..37
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                                                                                                                                                            /note=
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                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%;
          "transmembrane beta-strand"
                                    "surface-exposed connecting
                                                           "transmembrane beta-strand"
                                                                                                                                                                                                           "transmembrane beta-strand"
                                                                                                                                                            "transmembrane beta-strand"
                                                                                                                                                                                   "surface-exposed connecting
                                                                                                           "surface-exposed connecting
                                                                                                                                    "transmembrane beta-strand"
                                                                                     "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                  therapy; vaccine; meningococcal B.
                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 824.5; DB 1/;
Pred. No. 2.4e-82;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                     beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 175
                                                                                                                                                                                   loop"
                                                                                                            loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The isolated
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RESULT 6
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AC AAR7
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                                                                                                                                                                                                                                                      Matches
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Best Local (
                         AAR73911;
  05-DEC-1995
                                             AAR73911 standard;
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                   species. A claimed composition includes the NspA protein, preferably in mature form. The compositions are used e.g. as immunogenic compositions, recines or diagnostic reagents. They are used to treat or prevent Neisserial infection, to detect the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria, and/or as reagents which can raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                        combination compositions comprising: (i) 2 or more Neisserial proteins, (ii) 2 or more different Neisserial nucleic acids; or (iii) mixtures of 1 or more Neisserial protein and 1 or more Neisserial nucleic acids are Neisserial nucleic acid. The proteins and nucleic acids are preferably from different Neisseria spp., especially Neisseria meningitidis and Neisseria gonorrhoeae, but may be from the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developed as a vaccine for the prevention of meningococcal disease caused by all serotypes. The invention provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giuliani MM, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein, which contains 8 transmembrane beta-strands surface-exposed connected loops. Recombinant NspA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the Neisseria meningitidis NspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Fig 32; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition comprising first and second biological molecules from Neisseria bacterium, useful as vaccines or immunogenic compositions for treating Neisserial infections \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-025167/03.
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19-AUG-1999;
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                                                                                                                                                                                                                                                                                                                           against Neisserial bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
                                                                                                          121
                                                                                                                                  140
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                                                                                                          NVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 155
                                                                                                                    NVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                       LYSIGASAIYDFDTQSPYKPYLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTP 120
                                                                                                                                                                     LYSIGASAIYDEDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTP
                                                                                                                                                                                                     EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 60
                                                                                                                                                                                                                  EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 79
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                    155 AA;
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0005730
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-0011692
99GB-0019705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "1
131..145
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146..155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                              protein; 170
                                                                                                                                                                                                                                                  90.4%; Score 785; DB 22;
100.0%; Pred. No. 4.4e-78;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "surface-exposed connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant NspA is being
                                                                                                                                                                                                                                                                           Length 155;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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                                                                                                                                                                                                                                                                                                              Matches
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        Proteinase
                                N. meningitidis 608B peptide CS-857.
                                                                                                       AAW04912 standard; Protein; 25
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sharma LR,
                                                       22-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viral.
                                                                                                                                                                  135
                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                              41;
        K reistant;
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AAR73911 is the Neisseria meningitidis opacity related protein POPM3. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73889 and AAR73901, which are recognised by a monoclona antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis treatments. The peptides may also be used as vaccines against meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide(s) and corresp. antibodies for the treatment of meningitis - the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 47; Fig 5/10; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis; opacity related protein POPM3; vaccine; meningitis related homologous antigenic sequence; MRHAS; RV-1; limmunoassay; diagnosis; treatment; prophylactic; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting and preventing meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-147431/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NB: Identified by matching corresponding MRHAS peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAR/) SHARMA L R. (VALS/) VAN ALSTYNE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                           15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                          80 LYSIGASATYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                 46 FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                        6 ATLIALALPAAALAEGASGFYVQADAAH-----AKASSSLGS-----AKG 45
ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
                                                                                                                    IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Alstyne
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0127499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-CA00516
                                                                                                                                                                                                                                                                                                                                                                                                   15.6%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                Score 135; DB 16;
Pred. No. 9.4e-07;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POPM3
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 170;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                 --KAPSTDFK 79
                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                               Gaps
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4.

Neisseria meningitidis; epitope; mapping; antibody; detection; probe; surface protein.

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RESULT 8
AAU34556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                              21-MAY-2000;
23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9 describes the epitope mapping of the 22 kD N. meningitidis protein. Identification was accomplished using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against
or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 84; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brodeur BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1995;
17-MAR-1995;
                Haselbeck R, Yamamoto RT,
                                                                                                                 23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                              WO200170955-A2
                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                     antibiotic;
                                                                                                                                                                                                                                                                                                                                                              E. coli cellular proliferation protein #137.
                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU34556 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IAFB-) IAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                       21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic cellular proliferation protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9629412-A1
                                                          (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FAVDYTRYKNYKAPSTDFKLYSIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIO VAC INC
                                                                                                                                            2000US-191078P.
2000US-206848P.
2000US-207727P.
                                                                                                                                                                                                                                                                                                                    antibacterial; drug design.
                                                                                     2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamel J,
                Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0001983.
95US-0406362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-CA00157
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martin D,
                             Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 133; DB 17; Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rioux C;
                             Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunisation against,
                             Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                             Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                       RESULT 9
AAB47447
ID AAB4
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                                                                                                                                                                                                                                                                                                                                                Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to C prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential C genes, their use in the discovery of novel antibiotics, the essential C genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella C pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The C invention is also useful for the identification of potential new targets of antibiotic development. The antisense nucleic acids can also be used C to identify proteins used in proliferation, to express these proteins, C and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence is also useful to screen CC a wide variety of organisms. The present sequence represents an CC wide variety of organisms. The present sequence represents an CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                         Key
Domain
                                                                                                                            surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitop otitis media; sinusitis; conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the printed specification, but was obtained in electronic format directly from WIPO at ftp. winc int /chiz /chiz /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611495/70.
N-PSDB; AAS52415.
                                                                                                                                                                                        MOMP P5
                                                                                                                                                                                                                   31-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3;
 Domain
                                                                                   Haemophilus influenzae.
                                                                                                                                                                                                                                              AAB47447;
                                                                                                                                                                                                                                                                         AAB47447 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                              lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                169
                                                                                                                                                                                                                                                                                                                                                                                                        109
                                                                                                                                                                                                                                                                                                                                                                           141 -- VDLDAGYRYNYIGKVNTVKNVRSG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKALATLIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RINDLRFAVDYTRYKNYKA-----PSTDFKLYSIGASAIYDF------
                                                                                                                                                                                                                                                                                                                                               WLVNMSVWYM-----DIDTTANYKLG 189
                                                                                                                                                                                                                                                                                                                                                                                                      YFGDASSKFRPYVGAGINYTTFFDNGFNDHGKEAGLSDLSLKDSWGAAGQVGVDYLINRD
                                                                                                                                                                                                                                                                                                                                                                                                                                ---DTQSPVKPYLGARLS------LNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TNNTQLGLTFT----YMATDNIGVELLAATPFR-HKIGTRATGDIATVHHLPPTLMAQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKKLTVAALAVTTLLSGSAFAHEAGEFFMRAGSATVRPTEGAGGTLGSLGGFSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq ID No 10149; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                 (first entry)
/label= Loop 1
/note= "Extracellular domain"
89..100
                                         Location/Qualifiers 38..57
                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%;
23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94.5; DB Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212;
                                                                                                                                           epitope
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Gaps

10;

54

91 54

168

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                                                            AAU38252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein may be replaced with a modified peptide of the invention. Each of these peptides contain an LBI(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP P5 from strain ntHi1128, representing amino acids Arg117 to Gly135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native
                AAU38252;
                                            AAU38252 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          environment in the recombinant outer membrane protein. The modi-
MOMP P5 may be used to induce an immune response in a mammal to
prevent or treat Haemophilus influenzae infection or associated
disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the major outer membrane protein P5 of non-typeable H. influenzae. One or more surface exposed loops of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otitis media and conjunctivitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berthet FJ, Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-2000; 2000GB-0003502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2001; 2001WO-EP01556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200161013-A1
                                                                                                                     181 LTRVGKYRPQDKPNTALNYNPWIGSINAGISYRF 214
                                                                                                                                                                          121 DYYGKAGVALVRSDYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLEYQW
                                                                                                                                                                                                                                        61
                                                                                                                                                                                                        98 KPYLGARLSLNRASVDLGGSDSFSQTSIG-----LGVL-TGVSYAVTPNVDLDAGY-- 147
                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                  48 PRISAGYRI----NDLRFAV-----DYTRYKNYKAPSTDFKLYSIGA--SAIYDFDTQSPV 97
                                                                                                                                                                                                                                                                                              1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQASFHDGLRALAREYKVGYHRNSFT 60
                                                                                                                                                                                                                                                                                                                           1 MKKALATLIALALPAAALAEGA---SGFYYQADAAHAKASSSLGS------AKGFS 47
                                                                                                                                                                                                                                       YGVFGGYQILNQNNLGLAVELGYDDFGRAKGREKGKTVVKHTNHGTHLSLKGSYEVLEGL
                                                                                                                                                ----RYNYIGKVNTVKNVRS--GELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     353 AA;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Loop 3
/note= "Extracellular domain"
181..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Extracellular domain"
136..150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Loop
                                                                                                                                                                                                                                                                                                                                                                      10.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poolman J, Thonnard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loop 4
                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                      Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                            A
                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                                                                                                                                                    Length 353;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The modified
                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify mortalis used to make the process of the contract of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Seq ID No 13845; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antihinties, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhi cellular proliferation protein #143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC
135 YFGDSSSKVRPYVGVGVNYTTFFDNDFNDNGKKTGLSDLSFKDSXGAAGQVGVDYLINRD
                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                    1 MKKALATLIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                     ---DTQSPVKPYLGARLS-----LNRASVDLGGSDSFSQTSIGLGVLTGVSYAVT--
                                                                                                                --NNTQLGLTFT----YMATDNIGVELLAATPFR-HKVGTGATGDIATVHLLPPTLMAQW 134
                                                                                                                                                                      RINDLRFAVDYTRYKNYKA------PSTDFKLYSIGASAIYDF----
                                                                                                                                                                                                                           MKKFTVAALALTTLLSGSAFAHEAGEFFMRAGPATVRPTEGAGGTLGHLNGFD--VS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen
                                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind
                                                                                                                                                                                                                                                                                                                                                                       Score 89.5; DB Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick JD,
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                               Length 257;
                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    · of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                              81
                                                                                                                                                                      91
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139

-----PNVDLDAGYRYNYIGKVNTVK 159

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RESULT 11
AAY84612
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                                                                                                                                     Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                The present sequence represents an outer membrane protein 21 (OMP21) of Moraxella catarrhalis strain ATCC49143. The OMP21 protein has an apparent molecular weight of 16-20 kD as determined by sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE). OMP21, its nucleic acids and antibodies can be used in prophylactic and therapeutic compositions for treating a M. catarrhalis bacterial infection, otitis media, respiratory infections, sinusitis and pneumonia. They are useful as reagents for the clinical or medical diagnosis of M. catarrhalis infections and for scientific research on the properties of pathogenicity, virulence and infectivity of M. catarrhalis and host defence mechanisms. The antibodies, particularly those that are cytotoxic may be used in passive immunisation to prevent or attenuate M. catarrhalis infections of animals e.g. humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane protein 21; OMP21; strain ATCC49143; bacterial infection; otitis media; respiratory infection; sinusitis; pneumonia; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY84612 standard; Protein; 180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated outer membrane protein from a Moraxella catarrhalis strain used for diagnosis treatment and prevention of disease caused by M. catarrhalis e.g. pneumonia, otitis media and respiratory infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 4; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA12591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ANTE-) ANTEX BIOLOGICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
60
                                53
GYNF-DQNFGVEAEFVGSDAKEFNAGVSPVKGDVKSFGAYGTYRYNFINTPF--YAKGKL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-293149/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WLIGASVWYMDIDTTANYKMGGVQQHDSVR 224
                            GYRINDLRFAVDY----TRYKNYKAPSTDFK--LYSIGASAIYDFD-TQSPVKPYLGARL 105
                                                                                  KALATLIA-----LALPA-AALAEGASGF---YVQADAAHAKASSSLGSAKGFSPRISA 52
                                                                KTLKTLLAVSASSLLAMSANAAISYGNSADAQPYVGAKIGQVDAKQINGKNTAYG--IYA
                                                                                                                                                       Similarity
                                                                                                                                                                                                         180 AA;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0164714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US22918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Ala encoded by CCC"
                                                                                                                                                     10.2%; Score 88.5; DB 21; 26.7%; Pred. No. 0.13;
                                                                                                                                     29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 of strain ATCC49143
                                                                                                                                     75;
                                                                                                                                     Indels
                                                                                                                                                                     Length 180;
                                                                                                                                     39;
                                                                                                                                 Gaps
                                                                  59
                                                                                                                                     13;
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8 LIALALPAAA-LAEGASGFYVQADAAHAKASSSLGSAKGFSPR-----ISAGYRINDL 59

Query Match Best Local Similarity

10.2%;

Score 88.5; DB Pred. No. 0.15; Mismatches

Matches

Conservative

35;

65; 20;

Indels 41; Length

Gaps

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RESULT 12
AAY34533
ID AAY34
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                                                                                                                                                                                                                                                                                                                                   09-APR-1998;
23-APR-1998;
05-MAY-1998;
                                 Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY3483. AAY91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                               Agius CT,
Ross BC,
                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1997;
31-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; antigenic.
Sequence
                                                                                                                                               Claim 1; Page 524; 588pp; English.
                                                                                                                                                                       gingivitis
                                                                                                                                                                                                                                                                                                            22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphorymonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY34533 standard; Protein;
                        especially gingivitis.
                                                                                                                     AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                   Antigenic Porphorymonas gingivalis peptides for
                                                                                                                                                                                                                                                                                   (CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9929870-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphorymonas gingivalis protein PG64.
                                                                                                                                                                                                                                                                                                                                                                       10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 SLNRASVDLGG------SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                        1999-385613/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIAKTKYDVTSRNATTYSNKSDKTSLAGGV--GVGFKPLANVGVEAS--YNYLSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --DANAISLGAHLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                               Rothel LJ,
                                                                                                                                                                                                                                                           Barr IG,
204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis.
                                                                                                                                                                                                                                                                                                                                               98AU-0002264.
98AU-0002911.
98AU-0003128.
                                                                                                                                                                                                                                                                                                           98AU-0003338.
98AU-0003654.
98AU-0004917.
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                                                                                                                                                                                                                                                                                                                                                                                                              97AU-0000839
                                                                                                                                                                                                                                                                                                                                                                                                                        98AU-0005028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                              Hocking DM,
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA
                                                                                                                                                                                                                                                           Margetts
                                                                                                                                                                                                                                                           MB,
                                                                                                                                                                                 preventing
                                                                                                                                                                                                                                                           Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
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RESULT 13
AAY34400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                            AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX94318 to AAX94583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation
                                                                                                                                                Claim 1; Page 371; 588pp; English.
Sequence
                                    assays.
                                                                                                                                                                                     Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY34400 standard; Protein; 221 AA.
                       especially
                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                  Ross
                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                               09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1997;
31-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphorymonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphorymonas gingivalis protein PG64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY34400;
                                                                                                                                                                                                              N-PSDB; AAX91618.
                                                                                                                                                                                                                                                              Agius CT,
                                                                                                                                                                                                                                                                                      (CSLC-) CSL
                                                                                                                                                                                                                                                                                                                29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                    23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                            10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 F 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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                                                                                                                                                                                                                           1999-385613/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNRFDLGLGLSAALSY---DRYYVQIGYEH----GLLNMLKDAPDKTSLRNHDFFVGLGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK-----NVRSGELSVGVRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVGLRVGAAAEFALSNDGFYLAPGLAYTMRGAKMESLSETTTRLHYLQIPVNAGMRFS--
                                 Porphorymonas gingivalis
                                                                                                                                                                                                                                                  Rothel LJ,
                    gingivitis.
 221
                                                                                                                                                                                                                                                              Barr IG,
                                                                                                                                                                                                                                                                                       LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                         98AU-0002264.
98AU-0002911.
98AU-0003128.
98AU-0003338.
98AU-0003654.
                                                                                                                                                                                                                                                                                                                                                                                     97AU-0000839.
97AU-0001182.
98AU-0001546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-AU01023
                                                                                                                                                                                                                                                Hocking DM, Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·DNMAISLEAGPYFAYGVAGTIK - - - - TKVAGVTASVDAFGDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              periodontal disease; gingivitis;
                                   is involved in periodontal disease
                                                                                                                                                                                                                                                             Margetts MB,
                                                                                                                                                                                                                                                               Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
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Query Match

10.2%;

Score

88.5;

DВ 20;

Length 221

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                          This represents a UspA2 antigen of Moraxella catarrhalis strain 035E. Nucleic acid sequences encoding the UspA1 and A2 antigens of M. catarrhalis isolates 035E, 046E, TTA24 and TTA37 can be used in genetic vaccination. An antigenic composition or vaccine containing antigenic peptides from UspA1 or UspA2 antigens are used to induce an immune response in mammals against M. catarrhalis and can be used to the provided of the containing and the containing and the containing and the containing the cont
   sequences are also used to produce recombinant proteins and for screening for potential anti-M. catarrhalis agents, while their fragments are
                                                       are useful for passive immunisation and as immunoassay reagents. Detection of the epitopic core sequence, by immunoassay or by PCR, is used to diagnose infection. The Usp antigens encoding nucleic acid
                                                                                                                                                  treat infections such as otitis media, sinusitis, lower respiratory tract infections. They can also be used as immunity enhancers for other bacterial, parasitic or viral antigens, to raise antibodies and as immunoassay reagents for detecting specific antibodies. The antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 24; Pages 138-140; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV41342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW68202 standard; Protein; 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catarrhalis infection, and antibodies for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide(s) containing the core epitope of Moraxella catarrhalis Usp proteins - useful in, e.g. vaccines to prevent or treat M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-377595/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maciver I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aebi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis; UspA1; UspA2; antigen; vaccine; otitis media; sinusitis; lower respin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 F 174
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potential anti-M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
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catarrhalis agents, while their fragments are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sinusitis; lower respiratory tract infection;
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35; Mismatches
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This represents a UspA2 antigen of Moraxella catarrhalis strain TTA24.

Nucleic acid sequences encoding the UspA1 and A2 antigens of
M. catarrhalis isolates O35E, 046E, TTA24 and TTA37 can be used in
C m. catarrhalis isolates O35E, 046E, TTA24 and TTA37 can be used in
C enetic vaccination. An antigenic composition or vaccine containing
C antigenic peptides from UspA1 or UspA2 antigens are used to induce an
C immune response in mammals against M. catarrhalis and can be used to
C treat infections such as otitis media, sinusitis, lower respiratory
C tract infections. They can also be used as immunity enhancers for other
C bacterial, parasitic or viral antigens, to raise antibodies and as
C immunoassay reagents for detecting specific antibodies. The antibodies
C are useful for passive immunisation and as immunoassay reagents.
C Detection of the epitopic core sequence, by immunoassay or by PCR, is
C used to diagnose infection. The Usp antigens encoding nucleic acid
C sequences are also used to produce recombinant proteins and for screening
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                                                                                                                                                                                                                                                                                                       New peptide(s) containing the core epitope of Moraxella catarrhalis Usp proteins - useful in, e.g. vaccines to prevent or treat M. catarrhalis infection, and antibodies for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-377595/32.
N-PSDB; AAV41346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis; UspAl; UspA2; antigen; genetic vaccination; vaccine; otitis media; sinusitis; lower respiratory tract infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. catarrhalis strain TTA24 UspA2 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW68206 standard; Protein; 610
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Search completed: October 28, 2002,
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Best Local
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                                                                                                                                                                                                                                                                                                           Sequence
                                             571 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIGVNYEF 610
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                                                                                                                                                                                                        19 AEGASGFYVQADA------AHAKASSSLGS-AKGFSPRISA-GYRIN--DLRFAVDY 65
                                                                          QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                              SKVENGMAAQAALSGLFQPYSVGKF------
                                                                                                                                           TRYKN----YKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFS 121
                                                                                                                                                                          ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAFDGRITALD 532
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Maximum DB seq length: 2000000000
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1 MKKALATLIALALPAAALAE......VNTVKNVRSGELSVGVRVKF
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/B_COMB.pep:*
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US-08-913-362-3
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US-08-913-362-8
US-08-913-362-26
US-08-482-847-20
US-08-487-997B-2
US-08-487-997B-2
US-08-487-722A-2
US-08-487-722A-2
US-09-336-447A-11
US-09-336-447A-15
US-09-336-447A-15
US-09-336-447A-15
US-08-813-362-15
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US-08-813-528-3
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NESULT1 US-08-13-56-2 JS-08-13-56-2 JS-08-13-562-2 JS-08-1	28 78.5 9.0 325 4 US-09-132-528-3 29 78.5 9.0 325 4 US-08-875-494-2 31 78.5 9.0 325 4 US-08-875-494-2 31 78.5 9.0 325 4 US-09-599-366-2 31 78.5 9.0 325 4 US-09-599-366-2 32 78.5 9.0 322 4 US-08-818-112-3 33 78.5 9.0 332 4 US-08-818-111-53 34 78.5 9.0 332 4 US-08-818-111-53 35 78.5 9.0 332 4 US-08-818-111-53 36 78.5 9.0 802 4 US-09-056-556-214 37 78 9.0 15 4 US-08-913-362-14 38 77 8 9.0 15 4 US-08-913-362-16 38 77 8 9.0 15 4 US-08-913-362-1 40 77 8.9 15 4 US-08-913-362-1 41 76 8.8 15 4 US-08-913-362-1 42 76 8.8 15 4 US-08-913-362-2 43 76 8.8 15 4 US-08-913-362-2 44 76 8.8 207 2 US-08-31-81-6 45 76 8.8 207 4 US-08-31-81-6 46 76 8.8 207 4 US-09-281-221-6 47 8-9 2123 4 US-09-281-221-6 48 8-9 207 4 US-09-281-221-6 49 Sequence 52, A Sequence 6, Ap
	Appli Appli Appli Appli Appli Appli Appl Appl

Query Match

100.0%;

Score 868;

DB 4;

Length 174;

Best Local Similarity

100.0%;

Indels

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                                                                            Query Match
Best Local Similarity
                                                              Matches
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-MAR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SQTSJGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0/
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                     TELEFAX:
1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                171;
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                                                                Conservative
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98.3%;
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                                                                               Score 854; DB 4;
Pred. No. 1.3e-91;
                                                                  Mismatches
                                                                                                DB 4; Length 174;
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Patent No. 6287574
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                                                                                                                                                                                 Matches 170;
                                                                                                                                                                                                               Query Match
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 17-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-NOV-
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                LENGTH:
                                             61 FAVDYTRYKNYKXAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 120
                                                                Local Similarity
                                                                                                               1 MKKALAXLIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
20007-5109
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Rioux, Clement
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(202)672-5399
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                   linear
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97.1%;
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121 FSQTSXGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175

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Sequence 4, Application US/08913362 Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            Matches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF MEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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TELEFAX: \"
904136
                                                                                                                                   121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                           121 SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                     61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
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                                                                                                                                                                                                                                                                                  1 MKKALATLIALALPAAALAEGASGYYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                               1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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Rioux, Clement
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Martin, Denis
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                              95.0%;
94.3%;
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RESULT 6
US-08-127-499A-20
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                                                                                                              Sequence 20, Application US/08127499A Patent No. 5510264 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%;
Best Local Similarity 95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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            APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARWA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-NUV-133,
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/406,362
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                      121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                           120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                   FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
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3000 K Street, N.W., Suite 500
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
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ADDRESSEE:

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Patent No.
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,847
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                 STREET: JULY
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                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                COUNTRY:
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CITY: Washington
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FILING DATE:
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5, 5556757
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3000 K Street, N.W., Suite 500
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(202)672-5399
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07-JUN-1995
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Brodeur, Bernal
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
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FILING DATE: U***...
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
NAME: 29,768
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    FILING DATE: 13-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
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REGISTRACION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 1
                                                                 FILING DATE: 17-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 04-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
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TELEFAX: 904136
                                                                                                                                                                                                                                                                                                                                                                      STATE: I
                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 17-MAR-1995
                                                                                                                                                                                                            APPLICATION NUMBER: US/08/913,362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109
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6287574
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US-09-336-447A-3
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US-08-913-362-26
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US-08-457-997B-2
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SEQ ID NO 3
LENGTH: 573
TYPE: PRT
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                                                                Sequence 2, Application US/08457997B Patent No. 5766608
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Best Local
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           GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis media Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/336,447A CURRENT FILING DATE: 1999-06-21 NUMBER OF SEQ ID NOS: 98
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APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
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LENGTH: 25 amino acids
TYPE: amino acid
NUMBER OF SEQUENCES:
                                                                                                                                                                             536 AIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIGVNYEF 573
                                                                                                                                                                                                      124 SIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                    481 --DTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSVGKFN---ATAALGGYGSKSAV 535
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                                                                                                                                                                                                                                                                                                                                                               AEGASGFYVQADA-----AHAKASSSLGS-AKGFSPRISA-GYRINDLRFAVDYTR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 133; DB 4; Similarity 100.0%; Pred. No. 5.2e-09;
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TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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NAME: GOLTICK, MATY E.
REGISTRATION UMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     APPLICANT: Kolattukudy, P. E. TITLE OF INVENTION: Otitis Media Vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
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                                                                                                                                            STATE: O
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CITY: Cleveland
                                                                                                                                                                                STREET: Suite 18 CITY: Cleveland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/457,997B
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                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAVLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
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                                                                                                                          'RY: U.S.A>
44114-2688
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44114-2688
ARE: PatentIn Release #1.0, Version #1.30 APPLICATION DATA:
                                                                                                                                                                 Ohio
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Suite 1800
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APPLICATION NUMBER: FILING DATE:

US/08/467,722A

CLASSIFICATION: 424

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US-09-336-447A-11
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APPLICANT: HANSEN, ERIC J.
APPLICANT: ACBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
APPLICANT: FREDENBURG, ROSS 
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
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Best Local S
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 610
TYPE: PRT
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LENGTH: 359 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
533 SKVENGMAAQAALSGLFQPYSVGKF--
                                                                                                                                                            473 ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAFDGRITALD 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 YAVLPELAVRLEYQWLTRYGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 YAVTPNVDLDAGY-----RYNYIGKVNTVKNVRS--GELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AYLSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 ARLSLNRASVDLGGSDSFSQTSIGL-----
                                                                                                                                                                                                                                           19 AEGASGFYVQADA-----AHAKASSSLGS-AKGFSPRISA-GYRIN--DLRFAVDY 65
                                                                                  66 TRYKN----YKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFS 121
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YRRNTFTYGV----FGGYQILNQD----NFGLAAELGYDDFGRAKLREAGKPKAKHTNHG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 YRINDLREAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL-----G 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 10.1%; Score 88; DB 3; Length 359; Local Similarity 22.7%; Pred. No. 0.048; les 52; Conservative 29; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG 53
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                  10.1%; Score 88; DB 4; Length 610. 26.0%; Pred. No. 0.11; tive 22; Mismatches 54; Indels
----NATAALGGYGSKS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Indels 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GVL-TGVS 134
                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Qy 122 QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
Db 571 AVAIGAGYRVNPNLAFKAGAAINTSGN-KKGSYNIGVNYEF 610
RESULT 13 US-09-336-447A-7
; Sequence 7, Application US/09336447A PARENAL TUROPHATION:
APPLICA APPLICA
MACIVER, ISOB FISKE, MICHAE
NVENTION: USPA1 AND ENCE: AMCY:024
ENT APPLICATION NUMBER OF SEQ ID NOS: 98
; TYPE: PRT ; ORGANISM: Moraxella catarrhalis US-09-336-447A-7
Query Match 10.1%; Score 88; DB 4; Length 624; Best Local Similarity 26.0%; Pred. No. 0.11; Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;
QY 19 AEGASGEYVQADAAHAKASSSLGS-AKGESPRISA-GYRINDLREAVDY 65
Qy 66 TRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFS 121
Db 547 SKVENGMAAQAALSGLFQPYSVGKFNATAALGGYGSKS 584
Qy 122 QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 :
RESULT 14 US-09-336-447A-15 ; Sequence 15, Application US/09336447A ; Patent No. 6310190
; GENERAL INFORMATION: ; APPLICANT: HANSEN, ERIC J. ; APPLICANT: AEBI, CHRISTOPH ; APPLICANT: COPE, LESLIE D. ; APPLICANT: MACIVER, ISOBEL
NT: FREDENBURG, ROSS A. FINVENTION: USPA1 AND USPA2 AN FERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/99/356,44/A CURRENT FILING DATE: 1999-06-21 NUMBER OF SEQ ID NOS: 98 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 15 LENGTH: 889
; ORGANISM: Moraxella catarrhalis US-09-336-447A-15
Query Match 10.1%; Score 88; DB 4; Length 889; Best Local Similarity 26.0%; Pred. No. 0.19; Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;

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밁
                                                                                                                                                                  ; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
US-08-913-362-15
                                               Q
Y
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US-08-913-362-15
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                                                                           Query Match 10.0%; Score 87; DB 4; Length 16; Best Local Similarity 100.0%; Pred. No. 0.0006; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
TELEX: 904116
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08913362
Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          850 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIGVNYEF 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812 SKVENGMAAQAALSGLFQPYSVGKF--------NATAALGGYGSKS 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                752 ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAFDGRITALD 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TRYKN----YKAPSTDFKLYSIGASATYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AEGASGFYVQADA------AHAKASSSLGS-AKGFSPRISA-GYRIN--DLRFAVDY 65
                                                                             0;
                                                                             Gaps
                                                                           0,
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Search completed: October 28, 2002, 16:04:18 Job time: 11.4864 secs

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OM protein - protein search, using sw model
                                                                                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Title: Perfect score:

Run on:

Sequence: US-09-684-883-2 868 1 MKKALATLIALALPAAALAE......VNTVKNVRSGELSVGVRVKF 174

October 28, 2002, 15:58:04 ; Search time 12.4921 Seconds (without alignments) 1339.485 Million cell updates/sec

Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM62

283138 segs, 96089334 residues

283138

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : <u>*</u> 3 2 1 PIR_71:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	⊢	No.	Result	
215	217	219	221	224.5	226	226	226	226	231	232	232	232.5	232.5	236	236.5	237	237	238	239	240.5	240.5	241	241	241.5	242	244.5	854	864	Score	t	
24.8				25.9																	27.7				٠				Match	Query	di
239	178	238	248	243	261	238	234	234	233	234	234	282	234	283	268	270	254	258	266	257	237	260	258	338	260	261	174	174	Length		
2	N	N	N	N	N	N	N	Н	N	ν	N	N	N	N	_	N	N	N	N	N	N	Н	N	N	N	N	N	Ν	BB	1	
S28630	F64124	S36344	PL0038	S36346	S16619	S36349	S36348	KONH8	S36350	S36341	S36342	S16617	S36329	S72343	KONH2C	S04380	S20043	S08514	S16616	S16614	S36343	KONHO	S16612	S16613	S16611	S16610	B81932	G81174	ID		
	protein		protein		protein		protein	protein-	protein	protein	protein o	protein	protein	protein	protein	ty proteir			Description												

45	44	43	42 1:	41 1:	40 1:	39 1:	38	37	36	35	34 1	ω ω	32 1	31 2	30 2
									135						
14.0	14.1	14.5	14.6	14.6	14.9	14.9	15.2	15.6	15.6	16.2	17.3	20.7	21.8	23.4	23.7
264	284	192	201	70	284	281	239	170	168	187	210	121	235	214	247
N	N	N	2	N	2	N	N	N	N	N	N	N	Ν	Ν	N
I54668	AG3556	S44712	S16286	F64066	G98271	AH3012	AH0541	T10256	S08513	S20044	S77737	I64187	S44707	S44706	S28627
heat resistant agg	heat resistant agg	opacity protein op	opacity protein op	probable outer mem	hypothetical prote	outer surface prot			opacity protein-re						opacity protein op

ALIGNMENTS

RESULT 2 B81932 outer mem C; Species C; Date: 0 C; Accessi R; Parkhil ; Holroyd Nature 40 A; Title: A; Referen A; Referen A; Status:	Qy (Db (Qy 11)	Query M Best Lo Matches Qy 1	A; Reference A; Accession A; Status: p A; Status: p A; Molecule A; Rosidues A; Cross-ref A; Cross-ref A; Experimen C; Genetics: A; Gene: NMM	GB1174 outer me C;Special C;Date: C;Date: C;Access R;Tettel Hickey, ri, H.; Science A;Authou
RESULT 2 B81932 B81932 B81932 B81932 B81932 B81932 C;Bpecies: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: B81932 C;Accession: B81932 C;Accession: B81932 B;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More, Parkhill, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491 A;Reference number: A81775; MUID:20222556 A;Accession: B81932 A;Status: preliminary	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120	Query Match 99.5%; Score 864; DB 2; Length 174; Best Local Similarity 99.4%; Pred. No. 1.4e-70; Best Local Similarity 99.4%; Pred. No. 1.4e-70; Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60	A;Reference number: A81000; MUID:20175755 A;Recession: G81174 A;Accession: G81174 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-174 <ted: 1-174="" <ted:="" a;cross-references:="" a;experimental="" a;gene:="" a;residues:="" b,="" c;genetics:="" gb:ae002098;="" gb:ae002420;="" mc58="" nid:g7225876;="" nmb0663<="" pid:g722="" pidn:aaf41081.1;="" serogroup="" source:="" strain="" td=""><td>RESULT 1 RESULT 1 RESULT</td></ted:>	RESULT 1 RESULT

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F:76-84/Domain: transmembrane *Status predicted <TM2>
F:89-95/Domain: transmembrane *Status predicted <TM3>
F:99-134/Domain: extracellular *Status predicted <TM3>
F:90-134/Domain: extracellular *Status predicted <TM2>
F:102-129/Region: hypervariable region HV1
F:135-149/Domain: transmembrane *Status predicted <TM4>
F:155-165/Domain: transmembrane *Status predicted <TM5>
F:166-212/Domain: extracellular *Status predicted <TM5>
F:166-212/Domain: transmembrane *Status predicted <TM5>
F:113-225/Domain: transmembrane *Status predicted <TM6>
F:229-237/Domain: transmembrane *Status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;24-261/Product: opacity protein opak #status predicted F;34-42/Domain: transmembrane #status predicted <TM1> F;43-75/Domain: extracellular #status predicted <EXT1> F;51-61/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
S16610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain MS11, variant 4.8 A;Note: the authors did not translate the sequence for the signal peptide A;Note: expression of openity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Variety: strain MS11
C; Date: 13-Jan-1995 #sequence_revision 17-Oct-1997
C; Accession: S16610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Reywords: cell surface component; transmembrane protein F;1-10,11-23/Domain: signal sequence (fragments) #status |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam
A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-174 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84143.1; PID:g737957
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-261 <B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Bhat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opacity protein opaK precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N.Alternate names: outer membrane protein opaK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 닭
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S16610
                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: opacity protein
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Neisseria gonorrhoeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
        21
                                                    15 AAALAEG-ASGFYVQADAAHAKA-----SSSLGSAKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                       Госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nspA; NMA0862
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AQAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKGTTISTVSDYFRNIRTHSIHPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171;
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                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                              extracellular #status transmembrane #status
                                                                                                                                    28.2%;
29.9%;
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                                                                                                                                    Pred.
                                                                                                                                                          Score 244.5; DB 2;
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Pred. No. 1.1e-69;
                                                                                                           Mismatches
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                                                                                                                                    No.
                                                                                                                                                                                                              predicted
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                                                                                                                                 1.3e-14;
                                                                                                                                                                                                                                          <EXT4>
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                                                                                                        Indels
                                                                                                                                                          Length 261;
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                                                    ---FSPRI 50
                                                                                                        87;
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A; Nolecule type: DNA
A; Nolecule type: DNA
A; Nolecules: 24-260 <KUD>
A; Cross-references: EMBL: Z18937; NID: g49333; PIDN: CAA79370.1; PID: g940799
A; Cross-referental source: strain MS11, Variant F3
A; Note: expression of opacity proteins is regulated by the number of translated repea
A; Note: expression of opacity proteins is regulated by the number of translated repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Experimental source: strain MS11, variant 4.8
A)Note: the authors did not translate the sequence for the signal peptide
A)Note: expression of opacity proteins is regulated by the number of translated
of repeats place the start codon in frame with the rest of the protein
R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999 C;Accession: S16611; S36345; S28624 R;Bhart, KS.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc Mol. Microbiol. 5, 1889-1901, 1991 A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f A;Reference number: S16610; MUID:92114767 A;Recession: S16611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
S16611
                                                                                                                                                                                                                                                                                                 F;165-211/Domain: extracellular #status predicted <EXT3>F;170-217/Region: hypervariable region HV2
F;212-224/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                        F;95-133/Domain: extracellular #status predicted <EXT2>F;101-128/Region: hypervariable region HVI
F;104-148/Domain: transmembrane #status predicted <TM4>F;134-164/Domain: transmembrane #status predicted <TM5>F;154-164/Domain: trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;75-83/Domain: transmembrane #status predicted <TM2>
F;88-94/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: cell surface component; transmembrane protein F;1-10,11-23/Domain: signal sequence (fragments) #status | F;24-260/Product: opacity protein opaJ #status predicted |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: opacity protein
C;Keywords: cell surface compo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms A; Reference number: S36328; MUID:93178439
A; Accession: S36345
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A; Residues: 1-260 <BHA>
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C; Date: 04-T--
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N;Alternate names: outer membrane protein opa58
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                                                                                                                                                                                                         237-251/Domain:
                                                   Query Match
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Similarity

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A;Gene: opaB
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-13,14-104/Domain: signal sequence (fragments) #status
F;105-338/Product: opacity protein opaB #status predicted
F;115-133/Domain: transmembrane #status predicted CfMI>
F;115-133/Domain: transmembrane #status predicted CfMI>
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S16613
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A,Note: the authors did not translate the sequence for the signal peptide
A,Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opacity protein opaB precursor - Neisseria gonorrhoeae (strain MS11) (fragments) (C;Species: Neisseria gonorrhoeae A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 C;Accession: S16613
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                                                                                                                                                                                                                                                                                                                    F; 233-243/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;124-155/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X52373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-338 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam: A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                        F;224-289/Domain:
                                                                                                                                                                                                                                                                                                                                                           F;213-227/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                     F;176-212/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                         F;169-175/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;132-141/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S16613
                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                        290-302/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                249-295/Region:
                                                                                                                                                                                                                                                                                                                                                                               182-207/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 NTR-FKTHEASLGVRYRF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 GPGTTPTVYPGKNTQDAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 TENQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILH 185
  47
                                            97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKVNGNRTDRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKALATLIALALPAAALAEG---ASGFYVQADAAHA-----KASSSLGSAKGFS- 47
SPRISAGYRINDLRFAVDYTRYK - - NYKAPSTDFK
                                                                                 ALALPAAALAEG-ASGFYVQADAAHA-----KASSSLGS-----AKGF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLFAARAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKDKKSTVSDYFRNIRTHSI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKPSLLFSSALAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                     extracellular
                                                                                                                                                                                                                                                                                                                                                                             extracellular #status predicted hypervariable region HV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extracellular #status predicted <EXT1>
                                                                                                                                                                                                              transmembrane
                                                                                                                                                                                                                                     extracellular
                                                                                                                                                                                                                                                                                              hypervariable
                                                                                                                                                                                                                                                                                                                  transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane #status predicted transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   semivariable region
                                                                                                                                                                                                                                                      transmembrane
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                                                                                                                                                                                                                                                                                                                                                       transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVN 156
                                                                                                                                               27.8%;
                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                          #status predicted <TM8>
                                                                                                                                                                                                                            #status predicted <TM6>
#status predicted <TM7>
#status predicted <EXT4>
                                                                                                                                                                                                                                                                                              region HV2
                                                                                                                                                                                                                                                                                                               #status predicted
                                                                                                                                                 Pred.
                                                                                                                                                                Score 241.5;
                                                                                                                           Mismatches
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                                                                                                                                                 No.
                                                                                                                                               3.3e-14;
                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                  <TM5>
                                                                                                                                                                                                                                                                                                                                                           <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                               <TM2>
                                                                                                                           66;
                                                                                                                                                                                                                                                                                                                                                                                                                         <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                     <EXT2>
                                                                                                                           Indels
                                                                                                                                                                Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                           79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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F;88 94/Domain: transmembrane *status predicted <TM3>
F;98-131/Domain: transmembrane *status predicted <TM3>
F;95-131/Domain: extracellular *status predicted <TM4>
F;101-125/Region: hypervariable region HV1
F;132-146/Domain: transmembrane *status predicted <TM4>
F;152-162/Domain: transmembrane *status predicted <TM5>
F;163-209/Domain: extracellular *status predicted <EXT3>
F;163-215/Region: hypervariable region HV2
F;210-222/Domain: transmembrane *status predicted <TM6>
F;226-234/Domain: transmembrane *status predicted <TM7>
F;235-249/Domain: extracellular *status predicted <TM7>
F;250-258/Domain: transmembrane *status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: opaE
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
C;Heywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted cfMl>
F;24-258/Product: opacity protein opaE #status predicted cfMl>
F;34-42/Domain: extracellular #status predicted cEXTI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 5, 1889-1901, 1991
A,Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f A,Reference number: S16610; MUID:92114767
A,Accession: S16612
A,Rocession: S16612
A,Rosidues: 1-258 <BHA>
A,Residues: 1-258 <BHA>
A,Coss references: EMBL:X52369
A,Cross references: EMBL:X52369
A,Experimental source: strain MS11, variant 4.8
A,Note: the authors did not translate the sequence for the signal peptide
A,Note: expression of opacity proteins is regulated by the number of translated repea of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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R; Bhat, K.S.; Gibbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S16612
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                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNONKRDLKTENOENGTFHAV 216
                                                                                                                                                                                                                                                                                       KKALATLIALALPAAALAEG---ASGFYVQADAAHA----KASSSLGSAK-----
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NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGP 185
                                                                                                                YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                                                                                                           KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEEN
                                                           -----LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----LGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                   -GFSPRISAGYRINDLRFAVDYTRYK--NYKAPSTDFK-----
                                                                                                                                                                                                                                                                                                                                                                       27.8%;
29.7%;
                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                       Score 241; DB 2;
Pred. No. 2.6e-14;
                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <EXT4>
                                                                                                                                                                                                                                                                                                                                                                                                     Length 258;
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F;35-43/Domain: t
F;44-75/Domain: e
F;52-61/Region: s
F;76-84/Domain: t
F;102-129/Region: hypervariable region HV1
F;135-149/Domain: transmembrane #status predicted
F;155-15/Domain: transmembrane #status predicted
F;166-211/Domain: extracellular #status predicted
F;171-217/Region: hypervariable region HV2
F;212-224/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                   F:1-11,12-24/Domain: signal sequence (fragments) #status F:25-260/Product: opacity protein opac #status predicted F:35-43/Domain: transmembrane #status predicted <TMI>F:44-75/Domain: extracellular #status predicted <EXTI>F:52-61/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 25-260 <KUP>
A;Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
R;Meyer, T.F.
submitted to the EMBL Data Library, November 1992
A;Reference number: $28617
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A;Note: the authors translated the codon CCA for residue 32 as Thr
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO1. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A;Reference number: S16610; MUID:92114767
A;Accession: S16618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: opaC
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 25-260 <MEY>
A;Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 16-Jul-1999 (C;Accession: S16618; A24429; S36328; S28621 R;Bhat, K.S.; Gibbs, C.P.; Stern, W. S. S. Gibbs, C.P.; Stern, W. S. Gibbs, G.P.; Stern, W. S. Gibbs, G.P
                                                                                                                                                                                                                                                                                                    F;89-95/Domain: transmembrane #status predicted <TM3>F;96-134/Domain: extracellular #status predicted <EXT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Variable opacity (Opa) outer membrane proteins account A; Reference number: S36328; MUID:93178439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F. EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Stern, A.; Brown, J
Cell 47, 61-71, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Variety: strain MS11
C; Date: 31-Mar-1989 #s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S28621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
A; Residues: 25-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opacity protein opaC precursor - Neisseria gonorrhoeae (strain MS11) N;Alternate names: opacity protein VO; triosephosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S36328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A24429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A90887; MUID:87002493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X52370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 KNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 R-FKTHEASLGVRYRF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTPTVYPGKNTQDAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------SDSFSQTSIGLGYLTGYSYAVTPNVDLDAGYRYNYIGKVNTV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-260
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                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gonorrhoeae
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C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-237/Product: opacity protein opa57 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z18935; NID:g49331; PIDN:CAA79368.1; PID:g940797
A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment) N;Alternate names: outer membrane protein opa57
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                                                                                                                                                      F;142-188/Domain: extracellular F;147-194/Region: hypervariable F;189-201/Domain: transmembrane
                                                                                                                                                                                                                           F;111-125/Domain: transmembrane #status predicted F;131-141/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                               F;52-60/Domain: transmembrane *status predicted
F;65-71/Domain: transmembrane *status predicted
F;72-110/Domain: extracellular *status predicted
F;78-105/Region: hypervariable region HV1
                                                                                                                                                                                                                                                                                                                                                                           F;11-19/Domain: transmembrane *status predicted F;20-51/Domain: extracellular *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-237 < KUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms A; Reference number: S36328; MUID:93178439
A; Accession: S36343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C;Accession: S36343; S28626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Neisseria gonorrhoeae
                                                                                                                                    205-213/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 EASLGVRYRF 260
                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
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                                                                                                                                                                                                                                                                                                                                                      /Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 ATLIALPAAALAEGASGFYVQADAAHA------KASSSLGSAKGFS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKVLRTPGAHRESDSIRR--VGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --FKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD------LGG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PRISAGYRINDLRFAVDYTRY----
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                         Similarity
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29.6%;
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28.8%;
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                                                                                                                                                                                                  #status predicted <EXT3>
                                                                                                                                                                                                                      #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241; DB 1;
Pred. No. 2.6e-14;
                           Pred.
                                         Score 240.5;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                        predicted
                         No. 2
                                                                                      predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heuer,
                         .6e-14
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                                           DB 2;
                                                                                                                                                                                                                                                                                                                                    <TM2>
                                                                                                                                                                                                                                                                                                                                                                             <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I.; Meyer,
                                                                                                                                                                                                                                                                                                               <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                    <1M1>
                                                                                                                                                                                                                                                                                        <EXT2>
                                                                                                                                                         <9MT>
                                                                                                                                                                                                                                             <TM4>
                                                                                                               <EXT4>
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                                                                                                                                  <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indels
                                         Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                           <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KNYKAPSTD--
  85;
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
9;
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Qy 153 GKVN	Ξ
Db 186 AVTT	1
Ωу 108	LENKNQNKRDLKTE
Db 126 NIKT	
QÝ 70 NYKA	: : EHITHDYPEPTGTKKDKISTVSD
Db 66 YFRN	44
QУ 43	74; Conservative 26; Mismatches 72; Indels
Db 6 KKPS	27.7%; Score
Qy 2 KKAL	F;249-257/Domain: transmembrane #status predicted <ext4></ext4>
Matches 76	F;245-233/Domain: transmembrane #status predicted <tm6> F;225-233/Domain: transmembrane #status predicted <tm7> F:34-248 / Domain:</tm7></tm6>
Query Match	168-214/Region:
F; 243~257/Doma F; 258-266/Doma	F;132-146/Domain: transmembrane #status predicted <tm4> F:152-162/Domain: transmembrane #status predicted <tm5></tm5></tm4>
F; 234-242/Doma	F;101-126/Region: hypervariable region HV1
F;176-223/Regi	F;88-94/Domain: transmembrane *status predicted <tm2></tm2>
F; 160-170/Doma	F: 75-83/Domain: transportation for the first fi
F;140-154/Doma	F;43-74/Domain: transmembrane *status predicted <tm1></tm1>
F; 95-139/Doma	F:24-257/Product: opacity protein opaF #status predicted <sig></sig>
F;75-83/Domain	C; Keywords: cell surface component; transmembrane protein
F;51-60/Region	C;Superfamily: opacity protein
F; 34-42/Domai	the protein
F;1-10,11-23/ F;24-266/Prod	of repeats place the start codon in frame with the number of translated repeat e
C; Keywords: c	A; Note: the authors did not translate the sequence for the signal perfide
A; Gene: opaD	Exper
of repeats pl C;Genetics:	A;Residues: 1-257 <bha> A;Cross-references: EMBL:x52368</bha>
	A; Molecule type: DNA
	A; Reference number: S16610; MUID:92114767
A; Residues: 1 A; Cross-refer	מספסידיים איני איני איני איני איני איני איני א
	Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.
A; Reference n A; Accession:	C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 C;Accession: S16614
A; Title: The	
	. ~ .
C;Date: 04-Ju	RESULT 9
C; Species: Ne	ONDERSON ANALISADOVALKE ADJ
opacity prote	
RESULT 10	QY 117 SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
	Db 121 AVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNTQDAH 180
Db 245 KTF	VY 8/ AIYDFDTQSPVKPYLGARLSLNRASVDLGG 116
Qy 162 RSc	OF THE TENTH OF TH
Db 186 LNI	אַ נ
Оу 117	л h i
Db 126 NQ	

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y: opacity protein

cell surface component; transmembrane protein

3/Domain: signal sequence (fragments) #status predicted <MAT>

ain: transmembrane #status predicted <MAT>

ain: extracellular #status predicted <EXTI>

ion: semivariable region

ion: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in: transmembrane #status predicted <TM3>
ain: extracellular #status predicted <EXT2>
gion: hypervariable region HV1
main: transmembrane #status predicted <TM4>
main: transmembrane #status predicted <TM5>
main: transmembrane #status predicted <TM5>
main: extracellular #status predicted <EXT3>
gion: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al source: strain MS11, variant 4.8 authors did not translate the sequence for the signal peptide ession of opacity proteins is regulated by the number of translated repea place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsciol. 5, 1889-1901, 1991

opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f number: S16610; MUID:92114767
                                             TYPQNAASSVTTNAPIRKLPHHESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNW 245
                                                                                                 ----NRASV-----DLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYI 152
                                                                                                                                                                  TRKTEHRENGTFHAASSLGLSAVYDEDTGSRFKPYIGMRVAYGHVRHQVRSVQQETI 185
                                                                                                                                                                                                                         APSTDFK-----LYSIGASAIYDFDTQSPVKPYLGARLSL------ 107
                                                                                                                                                                                                                                                                                          NIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIKELLRNDNANSGGSHL 125
                                                                                                                                                                                                                                                                                                                                                                                                               SLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTAPKKAQLSTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LATLIALALPAAALAEG---ASGFYVQADAAHA------KASSSLGS- 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 27.5%; Score 239; DB 2; Length 266; Similarity 29.0%; Pred. No. 4.1e-14; 76; Conservative 26; Mismatches 70; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nain: transmembrane #status predicted <TM6>
nain: transmembrane #status predicted <TM7>
nain: extracellular #status predicted <EXT4;
nain: transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ein opaD precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPTVYTEENTQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-F 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGG 185
NTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rences: EMBL:X52372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ype: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                        ---AKGFSPRISAGYRINDLRFAVDYTRYK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              train MS1:
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                                                                                                                                                                                                                                                                                                                                                        ----- 69
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opacity protein related protein OPM1 precursor - Neisseria meningitidis (strain C1938)
N;Alternate names: outer membrane protein class 5
C;Species: Neisseria meningitidis
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F;100-124/Region: hypervariable region HV1
F;130-144/Domain: transmembrane #status predicted <TM4>
F;150-160/Domain: transmembrane #status predicted <TM5>
F;161-209/Domain: extracellular #status predicted <EXT3>
F;166-215/Region: hypervariable region HV2
F;166-215/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;50-59/Region: semivariable region
F;74-82/Domain: transmembrane #status predicted <TM2>
F;87-93/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: strain C1938
A, Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S08513; MUID:88260884
A;Accession: S08514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Stern, A.; Meyer, T.F. Mol. Microbiol. 1, 5-12, 1987
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C; Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-13,14-21/Domain: signal sequence (fragments) *status predicted <SIG> F;22-258/Product: opacity protein-related protein OPMI *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X06445; NID: g44906; PID: g1333787
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                            RESULT 12
S20043
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41 42 42
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opacity protein B precursor (clone pFLOB1700) - Neisseria meningitidis (strain FAM18) (f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210-222/Domain: transmembrane #status predicted <TM6>
226-234/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                         134 SSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPKGGTPAGGPVIK 193
                                                                                                                                             253
                                                                                                                                                                                                169 GVRVKF 174
                                                                                                                                                                                                                                                    194 TDPSKPPYHESHSISSLGLGVIAGYGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEASL 252
                                                                                                                                                                                                                                                                                                           118 -----DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 IHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKTEHQGNGSFHAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 FSPRISAGYRINDLRFAVDYTRYK-----L 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 LFSSAAQAASEDGSRSPYYVQADLAYAAERITHNYPEPTGADKDKISTVSDYFRNIRAHS 73
                                                                                                                                                                                                                                                                                                                                                                                                                   81 YSIGASAIYDFDTQSPVKPYLGARLSLNR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LIALALPAAALAEGASGFYVQADAAHA-------KASSSLGS------AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                             GMRYRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.4%; Score 238; DB 2
28.5%; Pred. No. 4.9e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ---ASVDLGGS----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Gaps
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A,Experimental source: strain FAM18; clone pFLOB1700
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A;Note: only a part of the translation is shown
A;Note: expression of opacity proteins is regulated by the number of translated repea of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Neisseria meningitidis
A;Variety: strain FAM18
C;Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 17-Oct-1997
C;Accession: S20043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: outer membrane protein class 5 C;Species: Neisseria meminqitia:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: cell surface component; transmembrane protein F;1-19/Domain: signal sequence (fragment) #status predicted <SIG>F;20-254/Product: opacity protein opaB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Characterization of the opa (class 5) gene family of Neisseria meningitidis. A,Reference number: S16286; MUID:92157869
A,Accession: S20043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: opaB
C; Superfamily: opacity protein
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                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;158-205/Domain: extracellular #status predicted <EXT3>F;163-211/Region: hypervariable region HV2
F;206-218/Domain: transmembrane #status predicted <TM6>
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F;40-69/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
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F;96-121/Region: hypervariable region HVJ
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                                                                                               192 STQNAYHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM
                                                                                                                                              119 -----SFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
                                                                                                                                                                                                     132 SLGLSAIYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVVTLTHGGADTKPTIYNGE 191
251 RYHF 254
                                                                                                                                                                                                                                                         82 SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL-------GGSD------ 118
                                                                                                                                                                                                                                                                                                                                                            12 LFSSAAQAASEDGSRSPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 71
                                                                                                                                                                                                                                                                                                          72 PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LIALALPAAALAEGASGFYVQADAAHA------KASSSLGS-----AKGFS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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28.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted <EXT2>
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                                                                                                                   250
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C;Species: Neisseria gonorrhoeae A;Variety: strain F62-SF C;Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998 C;Accession: S04380; S16504 R;Palmer, L.; Brooks, G.F.; Falkow, S.

opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fr

RESULT 13

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F:76-84/Domain: transmembrane #status predicted <TM2>
F:89-95/Domain: transmembrane #status predicted <TM3>
F:89-95/Domain: extracellular #status predicted <TM3>
F:96-141/Domain: extracellular #status predicted <EXT2>
F:102-136/Region: hypervariable region HV1
F:142-156/Domain: transmembrane #status predicted <TM4>
F:142-156/Domain: transmembrane #status predicted <TM5>
F:172-172/Domain: extracellular #status predicted <EXT3>
F:173-221/Domain: extracellular #status predicted <EXT3>
F:178-227/Region: hypervariable region HV2
F:222-334/Domain: transmembrane #status predicted <EXT3>
F:222-334/Domain: transmembrane #status predicted <EXT3>
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C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <
F;24-270/Product: opacity protein opak #status predicted <
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F;247-261/Domain:
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A; Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C; Genetics:
KONH2C
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                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: opaE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 259-270 <TAH>
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A; Accession: S16504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 3, 663-671, 1989
A;Title: Expression of gonococcal protein II in Escherichia coli by translational fusion A;Reference number: S04380; MUID:89343653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: translation not shown
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A; Residues: 1-270 < PAL>
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                                                                                                                                                                                                                                                               149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 HLNIQTQKTEHQENGTFHAASSLGLSTIYDFDTGSRFKPYIGARVAYGHVRHQVRSVEQE 185
                                                                                                                                                                                                                                                                                                                                                     186 TEIVTTYPKEQNVAPSPIPGAPTKKPAHHESRSISSLGFGAVAGVGIDITPNLTLDAGYR
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                                                                                                                                                                                                                                                      YNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYFRNIRTHSVHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELGRNDNSASGVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GF-----SPRISAGYRINDLRFAVDYTRYK------------
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27.1%;
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Pred. No. 6.3e-14;
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F;101-135/Region: hypervariable region HV1
F;141-155/Domain: transmembrane #status predicted <TM4>
F;161-171/Domain: transmembrane #status predicted <TM5>
F;172-219/Domain: extracellular #status predicted <EXT3>
F;177-225/Region: hypervariable region HV2
F;230-232/Domain: transmembrane #status predicted <TM6>
F;230-332/Domain: transmembrane #status predicted <TM6>
F;236-244/Domain: transmembrane #status predicted <TM6>
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F;88-94/Domain: transmembrane #status predicted <TM3>
F;95-140/Domain: extracellular #status predicted <EXT2>
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C;Keywords: cell surface component; transmembrane protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted
F;24-268/Product: opacity protein P.IIC #status experimental <MAT>
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C; Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
C; Accession: S03095; S16360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: outer membrane protein P.IIc C;Species: Neisseria gonorrhoon-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;51-60/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F; 43-74/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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A; Note: 241-Val was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-268 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol. 2, 797-806, 1988
A;Title: Three copies of a single protein
A;Reference number: S03095; MUID:89096501
A;Accession: S03095
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                                                                                                                                                                          193
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        253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 -GFSPRISAGYRINDLRFAVDYTRYK---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 SSLLFSSAARAASEDGGRGPYVQADLAYAAERITHDYPKPTGTGKNKISTVSDYFRNIRT 72
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TR-FKTHEASLGMRYRF 268
                                                                                VKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                  ---GGSDSFSQ-----TSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNT 157
                                                                                                                                                                                                                                                                                                                                   TEHQENGTFHAVSSLGLSTIYDFDTGSRFKPYIGMRVAYGHVRHQVRSVEQETEIITTYP 192
                                                                                                                                                             SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN 252
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semivariable region
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opacity protein

P.IIc precursor - Neisseria gonorrhoeae (strain JS3) (fragments)

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F;112-118/Domain: transmembrane #status predicted <TM3>F;119-155/Domain: extracellular #status predicted <EXTZ>F;119-155/Domain: hypervariable region HV1
F;156-170/Domain: transmembrane #status predicted <TM4>F;156-170/Domain: transmembrane #status predicted <TM4>F;176-186/Domain: transmembrane #status predicted <TM5>F;176-186/Domain: extracellular #status predicted <TM5>F;187-234/Domain: extracellular #status predicted <TM5>F;192-240/Region: hypervariable region HV2
F;235-247/Domain: transmembrane #status predicted <TM6>F;235-247/Domain: transmembrane #s
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C; Keywords: cell surface component; transmembrane protein
F;1-48, Domain: signal sequence #status predicted <SIG>F;49-283/Product: opacity protein opaH #status predicted <MAT>F;59-66/Domain: transmembrane #status predicted <TMI>F;58-66/Domain: extracellular #status predicted <ENTI>F;57-98/Domain: extracellular #status predicted <ENTI>F;75-84/Region: semivariable region
F;99-107/Domain: transmembrane #status predicted <TMI>F;99-107/Domain: tran
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R;Waldbeser, L.S.; Ajioka, R.S.; Merz, A.J.; Puaoi, D.; Lin, L.; Thomas, M.; So, M. Mol. Microbiol. 13, 919-928, 1994
A;Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in A;Reference number: S72343; MUID:95115561
A;Accession: S72343
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N;Alternate names: cell invasion protein opaH
C;Specias: Neisseria gonorrhoeae
A;Variety: isolate 15063G
C;Date: 14-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S72343
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A;Experimental source: isolate 15063g
A;Experimental source: asolate 15063g
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
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Search completed: October 28, 2002, 16:03:34
Job time: 14.4821 secs
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A; Residues: 1-283 <WAL>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                         171 RVKF 174
                                                                                                                                                                                                                                                                             280 RYRF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 SLGLSAVYDEKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKILTSFYGVATKPTTYDIGP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 PRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIERVQEAHSNRIDLKAENQENGTFHAVS 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAKG-----FS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
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27.9%;
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; Pred. No. 8.2e-14;
29; Mismatches 67
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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44; Search time 6.98996 Seconds (without alignments) 963.840 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 868
Sequence: 1 MKKALATLIALALPAAALAE......VNTVKNVRSGELSVGVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

105224

-processing: Minimum Match 0%

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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55 RINDLRFAVDYTRYKNY	17 ALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGY 54	Query Match 27.7%; Score 240.5; DB 1; Length 237; Best Local Similarity 29.6%; Pred. No. 4.4e-15; Matches 71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;	Z18935; CAA79368.1; Z8626; S28626; S28626; S28626; S28626; S28626; Opacity. ro; IPR003394; Opacity. pF02462; Opacity; 1. membrane; Multigene family; Signal. 1 1 1 POTENTIAL. 1 1 POTENTIAL. 2 >237 OPACITY PROTEIN OPAS7. RR 237 237 CE 237 AA; 26703 MW; F8B1A0FB5C7EECAD CRC64;	his SWISS-PROT entry is copyright. It is produced through a etween the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restrise by non-profit institutions as long as its content is odified and this statement is not removed. Usage by and notities requires a license agreement (See http://www.isb-sirsend.an email to license@isb-sib.ch).	UENCE FROM N.A. AIN-MS11 / F3; AIN-MS11 / F3; AIN-MS11 / F3; SCh EM., Knepper B., Kuroki T., Heuer I., Meyer T.F.; sch EM., Knepper B., Kuroki T., Heuer I., Meyer T.F.; riabble opacity (Opa) outer membrane proteins account for the pisms displayed by Neisseria gonorrhoeae for human leukocy thellal cells."; OJ. 12:641-650(1993). FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO VARIATION. SUBCELLULAR LOCATION: Outer membrane.	RESULT 1 OPAK_NEIGO STANDARD; PRT; 237 AA. ID OPAK_NEIGO STANDARD; PRT; 237 AA. AC Q04880; DT 01-OCT-1993 (Rel. 27, Created) DT 01-OCT-1993 (Rel. 27, Last sequence update) DT 01-WOV-1995 (Rel. 32, Last annotation update) DE Opacity protein OPA57 precursor (Fragment). OPAK. OS Neisseria gonorrhoeae. OS Neisseria gonorrhoeae. OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. OX NCBL_TaxID-485; RN [1]

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SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND REGIOUS OF HOMOLOGY WITH N.GONORRHOEAE (STRAIN MS11) OPA GENE
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Outer membrane protein P.IIC precursor (Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X12625; CAA31144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: THIS PROTEIN SERVES AS A PORIN
-1- SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 2:797-806(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van der Ley P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-JS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMPC_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMEM
158 VKNVRSGELSVGVRVKF
                                                  195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $03095; KONH2C.
rPro; IPR003394; Opacity.
; PF02462; Opacity; 1.
                                                                            ---GGSDSFSQ------TSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNT
                                                                                                                                            TEHQENGTFHAVSSLGLSTIYDFDTGSRFKPYIGMRVAYGHVRHQVRSVEQETEIITTYP
                                                SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN
                                                                                                                                                                                                                                       HSVHPRVSVGYDFGSWRIAADYARYRKWNNNKYSVSIKELLRNDNSASGVRGHLNIQTQK 134
                                                                                                                                                                                                                                                                                          -GFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                        SSLLFSSAARAASEDGGRGPYVQADLAYAAERITHDYPKPTGTGKNKISTVSDYFRNIRT
                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AA;
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26
36
77
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143
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222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270
44
85
96
157
173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.2%;
26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 236.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUTER MEMBRANE PROTEIN P.IIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F6B448373830A50D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                          -NYKAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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OPAC_NEIGO
                                                                                                                                              Matches
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account for the tropisms displayed by Neisseria gonorrhoeae for human leukocytes epithelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MS11 / VO;
MEDLINE=87002493; PubMed=3093085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA50 precursor (OPA30) (V0) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPAC.
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stern A., Brown M., Nickel P., Meyer T.F.; "Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria gonorrhoeae.
                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93178439; PubMed-8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=485;
 87
                              61
                                                                                                                 17
                                                                                                                                                            Local
                                                         55
                                                                                                                                                                                                                                                                                                   II; Z18927; CAA79360.1; -. 3; A24429; KONHO. 3; S28621; S28621; S28628. 3; S36328; S36328; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
AIYDFDTQSPVKPYLGARLSLN--RASVD
                                                                                                                ALAEGASGFYVQADAAHA------KASSSLGSAKGFS-----PRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47:61-71(1986).
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                              DFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENGSFHAVSSLGLS
                                                           RINDLRFAVDYTRY----
                                                                                    ASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRTHSIHPRVSVGY 60
                                                                                                                                                                                                                                                                                                                                                                             M14746; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                        PF02462; Opacity;
                                                                                                                                             70;
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                     236
236 AA;
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                          Multigene family; Signal
                                                                                                                                                                                                                  >236
236
                                                                                                                                                                                                      26685 MW; 68DC237692183398 CRC64;
                                                                                                                                                         27.1%;
29.3%;
                                                                                                                                           26;
                                                                                                                                                            Score 235; DB 1;
Pred. No. 1.4e-14;
                                                                                                                                                                                                                                 OPACITY PROTEIN OPA50.
                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no
                                                        ----KNYKAPSTD----FKLYSIGAS 86
                                                                                                                                                                        DB 1; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
                                                                                                                                              59;
                                                                                                                                              Indels
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OPAB_NEIGO
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01-OCT-1993
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epithelial cells.";
EMBO J. 12:641-650(1993).
-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
-PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q04874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPAB_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02462; Opacity; 1.
Outer membrane; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z18928; CAA79361.1; -. PIR; S28628; S28628. PIR; S36329; S36329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kupsch E.-M., Knepper B., Kuroki T., Heuer I., M
"Variable opacity (Opa) outer membrane proteins
tropisms displayed by Neisseria gonorrhoeae for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria gonorrhoeae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=485
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  182
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                                                                                                                                                                                                                                                                                                                                                  19 AEG-ASGFYVQADAAHA-----KASSSLGSAK---
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                FGGWRIAADYARYRKWNDNKYSYDIKELENKNQNKRDLKTENQENGTFHAVSSLGLSAVY
                                                                                                                                                                                                                                               INDLRFAVDYTRYK--NYKAPSTDFK-----------LYSIGASAIY
                                                                                                                                                                                                                                                                                                SEGNGRGPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESDSIRR---VGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF
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                                              SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                             DEKLNGKEKPYIGARVAYGHVRHSIDSTKKTTKELTSSYGGLNPTVYTEENTQNAHHQSN
                                                                                                                                               DFDTQSPVKPYLGARLSLN--RASVD------LGG----
                                                                                                                                                                                                                                                                                                                                                                                                   69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria;
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234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 27, Created)
(Rel. 27, Last seq
(Rel. 32, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPA51 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              >234
234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26772 MW; 9FFE5B5DABBA96CA CRC64;
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29.5%;
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Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 232.5;
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OPACITY PROTEIN OPA51.
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                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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tent is in no
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RESULT 7
OPAE_NEIGO
ID OPAE_N
AC Q04878
DT 01-OCT
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ID OPAJ_NEIGO
AC Q044882;
DT O1-OCT-1993
DT O1-OCT-1993
DT O1-CCT-1993
RR SEQUENCE FRC
RR STRAIN-M9311
RX MEDLINE-9311
RX MEDLINE-931
RT FUNCTION
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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01-OCT-1993 (Rel. 27, I
01-NOV-1995 (Rel. 32, I
Opacity protein OPA58 F
  Q04878;
01-OCT-1993 (Rel.
                                                             OPAE_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S28624; S28624.
InterPro; IPR003394; Opacity.
Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.";
                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane; Multigene family; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=485;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q04882;
01-OCT-1993
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
                                                                                                                                                                                               R--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                             QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 : | | : | | | : | | : | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI
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237 AA;
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                                                             STANDARD;
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OPACITY PROTEIN OPA58.
                                                       PRT;
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RESULT 8
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Best Local
                                                             Q04879;
01-OCT-1993 (Rel. 2
01-OCT-1993 (Rel. 2
01-NOV-1995 (Rel. 3
         Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                      Opacity protein OPA56 OPAF.
                                                                                                                OPAF_NEIGO
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SEQUENCE
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SIGNAL
CHAIN
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MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "variable opacity (Opa) outer membrane proteins account for the (tropisms displayed by Neisseria gonorrhoeae for human leukocytes epithelial cells.";
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01-NOV-1995 (Rel. 32,
Opacity protein OPA55
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-i- function: implicated in a number of adherence functions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-MS11 / F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                 KFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEENTQNAHHQSNSIRRVG
                                                                                                                                                                                                                                                             PVKPYLGARLSLN--RASVD-----LGG--
                                                                                                                                                                                                                                                                                     AADYARYRKWNDNKYSVDIKELENKNONKRDLKTENQENGTFHAVSSLGLSAVYDFKLND 127
                                                                                                                                                                                                                                                                                                                 AVDYTRYK -- NYKAPSTDFK ------
                                                                                                                                                                                                                                                                                                                                        GPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI 67
                                                                                                                                                                                 LGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVRYRF
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234 AA;
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                                                                                                                 STANDARD;
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Pred. No. 2.6e-14
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                                                                                                                 PRT;
          subdivision; Neisseriaceae;
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                                                 (Fragment).
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01-OCT-1993 (Rel. 27, Last sequence update)
01-NOY-1995 (Rel. 37, Last annotation update)
01-NOY-1995 (Rel. 37, Last annotation update)
Opacity protein OPA67 precursor (Fragment).
Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account fo tropisms displayed by Neisseria gonorrhoeae for human leuk epithelial cells.";
                                                                                                                                                                                                                                      OP67_NEIGO
Q05034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                            SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=485;
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                                                            MEDLINE=93178439; PubMed=8440254;
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InterPro; IPR003394; Opacity.
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS
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                                                                                                                                                                                                                                                                                                                                                               LGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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234 AA;
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28.9%;
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Pred. No. 2
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             human leukocytes and
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RESULT 10
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                       Stern A., Brown M., Nickel P., Meyer T.F. "Opacity genes in Neisseria gonorrhoeae: antigenic variation.";
                                                                                                                        Cell 47:61-71(1986)
                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
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CHAIN
                                                                                                                                                                                                                                 Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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P11297;
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Outer membrane; Multigene family; Signal.
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                                                                                             FUNCTION: IMPLICATED IN A NUMBER OF ADHIPROTEINS ARE IMPLICATED IN PATHOGENESIS
                                                                  SUBCELLULAR LOCATION: Outer membrane
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233 AA;
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Pred. No. 3
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OPACITY PROTEIN OPA67.
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                                                                                                                                                                     Meyer T.F.;
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OVT-1995 (Rel. 32, Last annotation updat)
Opacity protein OPA65 precursor (Fragment).
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                                                                                                                                                                                                                                                                                           MEDLINE-93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
                            EMBL; Z18940; CAA79373.1; -. PIR; S28617; S28617.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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              InterPro;
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                                                                                                                                                                                                                                   O J. 12:641-650(1993).
FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
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                                                                                                                                                                                                                         ARIATION
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             IPR003394; Opacity.
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Opacity;
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Last annotation update)
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 OP66_NEIGO
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                                     NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Opacity protein OPA66 precursor (Fragment).
Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            005033;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last seq
01-NOV-1995 (Rel. 32, Last ann
                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                         Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account for the tropisms displayed by Neisseria gonorrhoeae for human leukocytes
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               NON TER
                           CHAIN
                                                                   Outer membrane;
                                                                                Pfam; PF02462; Opacity;
                                                                                                                        EMBL;
                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                   EMBO
                                                                                                                                                                                                                                                                                                                                epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-VP1
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=485;
                                                                                             InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
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                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Outer membrane
                                                                                                                                                                                                                                                                                     ) J. 12:641-650(1993).
FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                             VARIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                           S28619; S28619
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                                                                                                                        Z18941; CAA79374.1; -.
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                                                                   Multigene
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              >238
238
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 26888 MW;
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Last annotation updat
                                                                   family; Signal
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Pred. No. 9.3e-14;
                         POTENTIAL.
OPACITY PROTEIN OPA66.
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B6E38AF1585263AA CRC64;
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                                                                                                                                                                                          as its content
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Query Match

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Score 226;

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RESULT 13
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                                                                    the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 This
                                EMBL; Z18939; CAA79372.1; -. EMBL; X60711; CAA43121.1; -.
                                                                                                                                                                                                                                                       Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F., Stern S., Kupsch E.-M., Meyer T.F., Swanson J.; Mol. Microbiol. 6:1073-1076(1992).

-i- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                 "The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of 11 complete genes."; Mol. Microbiol. 5:1889-1901(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92114767; PubMed=1815562;
Bhat K.S., Glbbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account fo
tropisms displayed by Neisseria gonorrhoeae for human leuk
epithelial cells.";
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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-MS11 / V18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGO
                                                                                                                                                                                                                                                                                                                        MEDLINE=92261323; PubMed=1584024;
                                                                                                                                                                                                                                                                                                                                                  ERRATUM
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Opacity protein
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                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                 S28631; S28631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. 12:641-650(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSPVKPYLGARLSLN--RASVD------LGGSD-----SFSQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPYVQADLAYAYEHITHDYPKPTDPSKGKLSTVSDYFRNIRTHSIHPRVSVGYDFGGWRI
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IPR003394; Opacity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta subdivision; Neisseriaceae; Neisseria
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Best Local
              NON_TER
                                                 InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restrict.
    CHAIN
                                    Outer membrane; Multigene family; Signal.
                                                                                                                                                                                                                                      epithelial cells.";
EMBO J. 12:641-650(1993).
-!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
                                                                                                                                                                                                                                                                                      STRAIN-MS11 / F3;
MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cropisms displayed by Neisseria gonorrhoeae for human leukocytes
                                                                                      EMBL; Z18938; CAA79371.1; -.
                                                                                                                  or send
                                                                                                                          entities requires a license agreement
                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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01-OCT-1993 (Rel.
01-NOV-1995 (Rel.
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SIGNAL
CHAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q04883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPAD_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                               OPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                        Opacity protein OPA59
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 DYQSNSIRRVGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AIYDFQINDKFKPYIGARVAYGHVRHSIDSTKKTIEVTTVPSNAPNGAVTTYNTDPKTQN 180
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                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Outer membrane.
                                                                            S28629; S28629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                              an email to license@isb-sib.ch).
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Last annotation update;
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                                                                                                                                                                                                                                                                                                                                                                                             beta subdivision; Neisseriaceae; Neisseria
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OPACITY PROTEIN OPA59
             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 226; DB 1;
Pred. No. 9.5e-14;
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SED -> MLKA (IN MS11 / V
V -> M (IN MS11 / V18).
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                                                                                                                   (See http://www.isb-sib.ch/announce/
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OPAI_NEIGO
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Query Match
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SEQUENCE
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Q04877;
Q1-0CT-1993 (Rel. 27, Created)
O1-OCT-1993 (Rel. 27, Last sequence update)
O1-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA54 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

"Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.";

EMBO J. 12.641-650(1993).

-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                EMBL; Z18931; CAA79364.1; -.
EMBL; Z18932; CAA79365.1; -.
EMBL; Z18632; CAA79365.1; -.
PIR; S28612; S28618.
PIR; S28618; S28618.
PIR; S36332; S36332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93178439; Pubmed=8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                   CHAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).

    -i- SUBCELLULAR LOCATION: Outer membrane.

                                                                  SEQUENCE
                                                                                                                                                                                                                             Outer membrane;
                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                        Pfam; PF02462; Opacity; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 VYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETIAVTTYPQNAASSVTTNAPIRKLPHH 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIATION.
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243 AA;
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                                                                                                                                                                                                                             Multigene family; Signal.
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27414 MW; 5930C73917436041 CRC64;
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                                                                        27488 MW; 968AB8603D961DD8 CRC64;
         25.8%;
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Pred. No. 1.3e-13;
         Score 224; DB 1; Length 244;
                                                                                                                                 POTENTIAL.
OPACITY PROTEIN OPA54.
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Matches 67; Conservative 25;
                                     117 SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                            128 AVYDEDTGSREKPYIGMRVAYGHVRHQVRSVQQETIAVTTYPQNAASSVTTNAPIRKLPH 187
188 HESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 244
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                                                                                                                   AIYDFDTQSPVKPYLGARLSL-----
                                                                                                                                                                                                                                                                                                                  Pred. No. 1.5e-13;
5; Mismatches 58
                                                                                                                          ------NRASV------DLGG 116
                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      88;
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search completed: October 28, 2002, 16:01:10
Job time : 8.98996 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
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868
1 MKKALATLIALALPAAALAE.....VNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     October 28, 2002,
                                                                                                                                                                                                                                                                                                                                                            SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                       sp_phage:*
                                                                                                                                                                                                                         sp_organelle:*
                                                                                                                                                                                                                                                                                                                           sp_bacteria:*
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                                                                                                                                                                                                                                                            sp_mammal:*
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                                                                                                                                                                                                                                                                                                                                            sp_archea:*
                                                                                                  sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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                                                                                                                                                                        sp_rodent:*
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SUMMARIES

Result	Score	Query Match	Query Match Length	BU	Ħ	Description
1	868	100.0	174	2	P96943	P96943 neisseria m
N	864	99.5	174	16	Q9RP17	Q9rp17 neisseria m
ω	857	98.7	174	2	Q9R2R1	neisseria m
4	854	98.4	174	16	P95372	P95372 neisseria m
ហ	852	98.2	174	N	Q9RP16	Q9rp16 neisseria m
6	846	97.5	174	N	Q9RP18	Q9rp18 neisseria m
7	825	95.0	174	N	P95343	P95343 neisseria g
œ	824.5	95.0	175	N	P95371	P95371 neisseria m
9	247	28.5	256	N	Q51124	Q51124 neisseria m
10	246.5	28.4	186	16	Q9CM19	Q9cm19 pasteurella
11	244	28.1	234	2	Q9R7I9	Q9r7i9 neisseria m
12	244	28.1	234	N	007280	007280 neisseria m
13	243	28.0	234	N	Q9R718	Q9r7i8 neisseria m
14	241.5	27.8	232	N	Q9K4T9	Q9k4t9 neisseria l
15	241.5	27.8	241	N	Q9AE80	Q9ae80 neisseria m
16	240 5	נ נ	220	N	098987	Q9r9a7 neisseria m

į	5	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
	226.5	N		27.	N	28.		w	w	•	32.	w	w	33.	233.5	w	ω	•	w	ω	•	w	ω	ω	38.	•	*	-	*
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	007279	033389	007278	031172	Q9K4T8	007273	Q9K4T7	030752	Q9K4T6	Q9R9A8	Q9R9A9	030753	Q9K4T5	Q51303	007912	Q51013	007925	007274	Q50943	Q9RQV4	Q9K4T3	338	031176	007287	Q50929	Q9R3P5	Q51125	Q51126	Q9K4T4
	727	3389	7278	1172	8	ω	4 t 7	030752	Q9k4t6	Q9r9a8					007912			007274	Q50943			3388	176	7287	929	r3p5	125	1126	k4t4
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ALIGNMENTS

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RESULT 1
P96943
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Query Match
Best Local Similarity
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EMBL; U52066; AAC35000.1; -.
EMBL; AF17568; AAD53286.1; -.
EMBL; AF175680; AAD53283.1; -.
EMBL; AF175682; AAD53285.1; -.
InterPro; IPR003394; Opacity.
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P96943;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97149429; PubMed=8996237;
Martin D., Cadieux N., Hamel J., Brodeur B.R.;
"Costimulation of T cell activation by integrin-associated protein (CD47) is an adhesion-dependent, CD28-independent signaling pathway.";
J. Exp. Med. 185:1-11(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NGP165, M986, AND NG6/88;
Moe G.R., Tan S., Granoff D.M.;
"Differences in Surface Expression of Neisserial Surface Protein among Neisserla meningitidis Group B strains.";
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                       Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                        174 AA;
                                                                                                                   19 P
18425 MW;
    100.0%;
                                                                                                                   POTENTIAL.
; E8B02767DDC6FE19 CRC64;
Score 868; DB 2; Pred. No. 2.7e-64;
                                     Length 174;
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RESULT
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STRAIN-MC58 / SEROGROUP B;

MEDLINE-20175755; PubMed=10710307;

MEDLINE-20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Hason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:1809-1815(2000).
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SEQUENCE FROM N.A.
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Neisseria meningitidis (ser
Bacteria; Proteobacteria; b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Differences in Surface Expression among Neisseria meningitidis Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moe G.R., Tan S., Granoff D.M.;
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                                    SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                           MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
   SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
                                                                                                                           FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                          MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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(TrEMBLrel. 19, Last annotation updat
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*Differences in Surface Expression among Neisseria meningitidis Grounds (1999).
Infect. Inmun. 0:0-0(1999).
EMBL; AR175679; AAD53280.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                       P95372
P95372;
01-MAY-1997
01-MAY-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrembLrel. 03, Created)
01-MAY-1997 (TrembLrel. 03, Last sequence update)
01-DEC-2001 (TrembLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN PRECURSOR.
MSPA OR NMA0862.
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Q9R2R1;
01-MAY-2000
01-MAY-2000
Parkhill J., Achtman M., James K.D., Bentley S.D., Churche Klee S.R., Morelli G., Basham D., Brown D., Chillingworth Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Whitehead S., Spratt B.G., Barrell B.G.,
                                                                                                                                                              Martin D., Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PFO
SEQUENCE
                                                                                                    STRAIN=Z2491 / SEROGROUP A / SEROTYPE MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                          STRAIN=24063;
                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                              Neisseria meningitidis, and
Neisseria meningitidis (serogroup
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Bacteria; Proteobacteria;
                                                                                                                                   SEQUENCE FROM N.A.
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174 AA; 18385 MW;
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                                                                                                                                                              l J., Rioux C., Br
EMBL/GenBank/DDBJ
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Last annotation updat
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Best Local :
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01-MAY-2000
01-JUN-2001
 Q9RP18;
01-MAY-2000
                        Q9RP18
                                                                                                                                                                                                                                                                                Moe G.R., Tan S., Granoff D.M.;
"Differences in Surface Expression of Neisserial Surface Protein among Neisseria meningitidis Group B strains.";
Infect. Immun. 0:0-0(1999).
EMBL; AF175681; AAD53284 1; -.
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                                                                                                                                                                                                                                                                                                                                           STRAIN-NG3/88;
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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EMBL; AL162754; CAB84143.1; --
EMBL; TRR003394; Opacity.
Pfam; PF02462; Opacity; 1.
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SIGNAL 1 19
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Nature 404:502-506(2000).
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                                                                                   SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                              FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                           MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                         SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                    PF02462;
ENCE 174
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2462; Opacity; 1.
174 AA; 18355 MW;
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(TrEMBLrel.
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                     PRELIMINARY;
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98.3%;
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Pred. No. 3.8e-63;
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Best Local
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SIGNAL
                                                                                                                                                                                Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                        MEDLINE-99270944; PubMed-10338491; Plante M., Cadieux N., Rioux C.R., Har "Antigenic and molecular conservation"
                                                                                                                                                                                                                                                                                                                      Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Differences in Surface Expression among Neisseria meningitidis Group Infect Immun. 0:0-0(1999).
EMBL; AF175676; AAD53279.1; InterPro; IPR003394; Opacity.
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                         Infect. Immun. 67:2855-2861(1999).
EMBL; U52069; AAB41581.1; -.
                                                                                                                                                                                                                                 protein.
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                             InterPro; IPR003394; Opacity.
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01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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      61
             61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                             Local
                                                   1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
                                              {\tt MKKALAALIALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGMRVKF 174
                                                                                                   164;
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                                                                                                                                               174 AA;
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174 AA; 18357 MW;
                                                                                                  Conservative
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18337 MW;
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97.1%;
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Last annotation update)
                                                                                                          Score 825; DB 2;
Pred. No. 9.5e-61;

    Mismatches

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                                                                                                                                              1B558EC8A040841A CRC64;
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ion of
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                                                                                                                    Length 174;
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GN Neis
CO Neis
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RN [1]
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01-MAY-1997
01-DEC-2001
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P95371;
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O51124;
O1-NOV-1996 (TrEMBLrel. O1, Created)
O1-MAY-1997 (TrEMBLrel. O3, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation updato)
OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99386904; PubMed=10456958; Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.; "Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein."; Infect. Immun. 67:4955-4959(1999).

EMBL; U52067; AAB41579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE PROTEIN PRECURSOR.
             Heckels J.E., Cannon J.G., Achtman M.;
"Recombinational reassortment among opa genes from ET-37 complex Neisseria meningitidis isolates of diverse geographical origins."
Microbiology 144:157-166(1998).
EMBL; U37255; AAC46101.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                              Neisseria meningitidis.
Bacteria; Proteobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-MCH 88;
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Bacteria; Proteobacteria; beta subdivision;
                                                                                                             Hobbs M.M., Malorny B., Prasad P.,
                                                                                                                              MEDLINE=98129089; PubMed=9467908;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=48
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   Pfam;
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 PF02462;
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   Opacity;
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18572 MW;
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95.4%;
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; D1EA8F2FF5CC2FEA CRC64;
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                                                                                                                 Morelli G., Kusecek B.,
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006143; AAK03109.1; -.
EMBL; IPR003394; Opacity.
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
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 178 AKVGLRYDF
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                                                                                                                                                      N
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                         LSVGVRVKF 174
                                                                                                  AMRLALDYTHYGKFSGTSYFGVNQKEHVSTKIYGLGLSAFYDFNINSVLKPYVGMRLASN 118
                                                                                                                                                    MKK---SLLVLAIGALCSLTASANFYVQGDLGVAKTKFSSYSEMNKTNIVPNVSVGYDLG 58
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                                                                           RASVDLGGSDSF---SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGE 165
                                                                                                                          DLRFAVDYTRYKNYKAPS-----TDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN 108
                                                  IFDIENKGSNFFRSEKTTKLGYGFIAGAQYGLMTNLFVNGGIEYNRLGRFSDT-SVNQYG
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 186
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28.3%;
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Pred. No. 8.
                                                                                                                                                                                                                            Score 246.5;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz B. Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S., Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M., "Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF001194; AAC32715.1; -. InterPro; IR003394; Opacity.
                                          Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                                                                         OPACITY PROTEIN (FRAGMENT).
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                   NCBI_TaxID=487;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02462; Opacity; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
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                                                                                                                                                                                                                                                                                                                                                                                       SSVGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGMRYHF 234
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Microbiol. 25:1047-1064(1997).
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                                       subdivision; Neisseriaceae;
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EMBL; AF001196; AAC32717.1; -.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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01-DEC-2001
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EMBL; AF001195; AAC32716.1; -.
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                                                      55 RINDLRFAVDYTRYK----NYKAPSTDFK-----
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                                                                                                                                                                                                                                                                                                                                                                                              IPR003394; Opacity.
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                                                                                                                                                                                                                                                                                                                  234 AA; 26191 MW; F01D3B9163066171 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TremBLrel. 13, Created)
(TremBLrel. 13, Last seq
(TremBLrel. 19, Last ann
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                     28.9%; Score 243; DB 2; 28.9%; Pred. No. 1.6e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%; Score 244; 28.9%; Pred. No. :
                                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             005AD356E93BCC50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seiler A., Wang J.F., del Valle J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
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                                                                                                                                                                                                                                                        DB 2; Length 234;
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59;
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                                                                                                                                                      ----FSPRISAGY
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                                                 -----LYSIGASAI 88
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RESULT
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AC Q9
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OC OC OC
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Best Local (
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Q9AE80;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toleman M.A., Aho E., Virji M.;
"Antigenic relatedness of commensal and pathogenic neisserial adhesins genetic and functional analyses of commensal Opa proteins.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ288888; CAB93949.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria lactamica
                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C501;
                       Neisseria meningitidis.
Bacteria; Proteobacteri
                                                            OPACITY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=486;
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NCBI_TaxID=487; [1]
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                                                                                                                                                                                    183
                                                                                                                                                                                                            122 QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDFKLNDKFKPYIGVRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSVGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGMRYHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDFDTQSPVKPYLGARLSLNR----
                                                                                                                                                                                      IRRVGFGAVAGVGIDITPNLTLDTGYRYHYWGRLENTR-FKTHEASLGMR 231
                                                                                                                                                                                                                                                   ASAIYDFDTQSPVKPYLGARLSLNR------
                                                                                                                                                                                                                                                                                                                                                           ATLIALALPAAALAEGASGFYVQADAAHAKASSSL----GSAKGFS----
                                                                                                                                                                                                                                                                                   SVGYDFGNWRIALDYARYNKWKHGKHIRTEQNKSVQNGTSVKLIADHTDKGTFKAESNYG
                                                                                                                                                                                                                                                                                                            SAGYRINDLRFAVDYTRYKNYK-----
                                                                                                                                                                                                                                                                                                                                    SSLLFSSAVQAANEDNGRGPYVQADLTYAYEHITHDYPGNNAKLFDDYRDVKTRSTHPRL
                                                                                                                                                                                                                                     ISAIYDFDTGTRFKPYVGARVGLGKIRHSIALEDKAEIIIGNIPSGGLKDAHPPIHESHS
                                                                                                                                                                                                                                                                                                                                                                                     70;
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                         Proteobacteria; beta
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14 >
232
232 AA;
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(TremBLrel. 15, Last sequence update)
(TremBLrel. 17, Last annotation update)
                                                                                                 (TrEMBLrel.
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14 >232
232
26094 MW; 3
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                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 241.5; DB 2
Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                           PRT;
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                         subdivision; Neisseriaceae;
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                                                                                                                                                                                                                                                            -----SDSFS
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Best Local
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Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo Popovic T., Schuurman I.G.A., Adegbola K.A., Zurth K., Gagneux S. Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis.
                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Z9620;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                          184
                                                                        118
                                                                                                     124
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                                                                                                                                                                                                                                                       16 AALAEGA-SGFYVQADAAHA-----KASSSLGS-----
                                                                                                                                                                                                                          4
                                                                                                                                                              DFGDWRIAADYASYRKWNDNKYSVNTKNVQVNKSNGNRQDLKTENQENGTFHAVSSLGLS 123
                                                                                                                                                                                            RINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                         AASEDGSRSPYYVQADLAYAAERITHDYPKASGANNTSTVSDYFRNIRAHSIHPRVSVGY 63
                                       YHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGVRYRF
                                                                                                                                                                                                                                                                                                                                                                                            AJ292238; CAC36361.1; -
Pro; IPR003394; Opacity.
                                                                       --DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNYRSGELSVGVRVKF 174
                                                                                                     AVYDENTGSREKPYAGVRVAYGHVRHSIDSTKKTTNVLTVPTNIPGGTPTIYNQGSTQDA
                                                                                                                                 AIYDFDTQSPVKPYLGARLSLN--RASVDL-
                                                                                                                                                                                                                                                                                     l Similarity
69; Conserv
                                                                                                                                                                                                                                                                                                                                               241 AA;
                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                   26923 MW;
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28.9%;
2002,
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Pred. No. 2.2
16:02:38
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1es 56;
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                                                                                                                                                                                                                                                                                                                    2;
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                                                                                                                                                                                                                                                                                          81;
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                                             241
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Search completed: October 28, Job time: 22.9713 secs

GenCore version 5.1.3
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A. Geneseq_032802:*

1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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Neisseria meningit
N. meningitidis 60
Salmonella typhi c
E. coli cellular p
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ein associ	AAB591	Ŋ	350	10.7	93.5	ω
Outer membrane pro	AAP82053	9	350	10.7	ω ·	~

ALIGNMENTS

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RESULT 1
AAW04892
ID AAW(
XX
Key
Peptide
                                        04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                     Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
       Brodeur BR,
                                                                                    26-SEP-1996
                                                                                                                            Protein
                                                                                                                                                                       Neisseria
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                       (IAFB-) IAF BIO VAC INC
                                                                                                    WO9629412-A1
                                                                                                                                                                                                                 Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                  15-MAR-1996;
                                                                                                                                                                      meningitidis strain MCH88
       Hamel J, Martin
                                                                                                                                                                                                                                  (first entry)
                                        95US-0001983
95US-0406362
                                                                  96WO-CA00157
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       Rioux C;
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Best Local
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                                                            04-AUG-1995;
17-MAR-1995;
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           Brodeur BR,
                                                                                                  15-MAR-1996;
                                                                                                                           26-SEP-1996
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N-PSDB; AAT39040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also be used to detect antibodies specific to N. meningitidis
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                                                                                                                                                                                                                                                                             gonorrhoeae;
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                                    BIO VAC INC
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           Hamel J,
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95US-0406362
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Pred. No. 2e-85;
Mismatches 0
           Rioux C;
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RESULT 3
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                                                         04-AUG-1995;
17-MAR-1995;
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strains - useful
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        Hamel J,
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95US-0406362
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97.1%;
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        Rioux C;
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ogenic Neisseria bacteria
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                    Brodeur BR,
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17-MAR-1995;
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strains - useful for prodn. of antibodies for immunisation against,
or diagnosis of, N. meningitidis infection
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DB; AAT39039.
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                  Hamel J, Martin
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                                                                                        95US-0001983
95US-0406362
                                                                                                                                               96WO-CA00157
                                                                                                                                                                                                                                                     /label= sig_peptide
20..174
/label= mat_protein
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.3%;
                                                                                                                                                                                                                                                                                                                                                                                             antibody; detection; probe; surface protein;.
                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis;
                                                                                                                                                                                                                                                   mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 824.5; DB 1
Pred. No. 3.9e-80;
                  Á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                  Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19895
ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    片
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis of by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis
Region
                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                    NspA; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis NspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB19895 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against
                                                                         Region
                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequences encoding the antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT39042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKALAALIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for the detection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; 117pp; English.
                                                                                                                                                  /note=
63..74
                                                                                                                                                                                        /note=
51..62
                                                                                                                                                                                                                           /note=
40..50
                                                                                                             /note=
78..88
                                                                                                                                                                                                                                                                 /note=
27..37
                                       105..114
                                                       /note=
                                                                                           /note=
                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                           104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.1%;
93.7%;
                                                                                       "transmembrane beta-strand"
               "transmembrane
                                                   "surface-exposed connecting
                                                                                                                              "transmembrane
                                                                                                                                                                                                        "transmembrane beta-strand"
                                                                                                                                                                                                                                         "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                     "transmembrane beta-strand"
                                                                                                                                                                "surface-exposed connecting
                                                                                                                                                                                                                                                                               "surface-exposed connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; vaccine; meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 813.5; DB 1
Pred. No. 5.9e-79;
2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or their fragments, can l
ogenic Neisseria bacteria.
                 beta-strand'
                                                                                                                              beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunisation against,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis or
                                                                                                                                                                    100p
                                                                                                                                                                                                                                                                               loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                   loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ₩.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
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RESULT 6
AAR73911
ID AAR7
XX
AC AAR7
XX
DT 05-D
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                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                  developed as a vaccine for the prevention of meningococcal disease caused by all serotypes. The invention provides combination compositions comprising: (i) 2 or more Meisserial nucleic acids; or proteins, (ii) 2 or more different Neisserial nucleic acids; or (ii) mixtures of 1 or more Neisserial protein and 1 or more Neisserial nucleic acids are preferably from different Neisseria spn., especially Neisseria meningitidis and Neisseria gonorrhoeae, but may be from the same species. A claimed composition includes the NBPA protein, preferably in mature form. The compositions are used e.g. as immunogenic compositions, vaccines or diagnostic reagents. They are used to treat or prevent Neisserial infection, to detect the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria, and/or as reagents which can raise antibodies
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1999;
19-AUG-1999;
09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition comprising first and second biological molecules from Neisseria bacterium, useful as vaccines or immunogenic compositions for treating Neisserial infections -
   05-DEC-1995
                                                         AAR73911 standard;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                against Neisserial bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, which contains \theta transmembrane beta-strands and 4 surface-exposed connected loops. Recombinant NspA is being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Fig 32; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200071725-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                       120
                                                                                                                                                                     140
                                                                                                                                                                                                   60
                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                              20 EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKQVPSTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is that of the Neisseria meningitidis NspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-025167/03
                                                                                                                                                                                                                 KLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDSFSQTSTGLGVLAGVSYAVT
                                                                                                                                                                     PNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                   KLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVT
                                                                                                                                                                                                                                                              EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYK-APSTDF 59
                                                                                                                                        PNVDLDAGYRYNY IGKVNTVKNVRSGELSVGVRVKF
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                    155 AA;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000GB-0005730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-IB00828
   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99GB-0011692.
99GB-0019705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "transmembrane beta-strand"
131..145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146..155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                          protein; 170 AA
                                                                                                                                                                                                                                                                                                                                     85.4%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "surface-exposed connecting loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rappuoli
                                                                                                                                                                                                                                                                                                                                     Score 746.5;
Pred. No. 7.3
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                  /.3e-72;
6;
                                                                                                                                        155
                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                    Length 155;
                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW04912
                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR73911 is the Neisseria meningitidis opacity related protein POPM3. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73889 and AAR7391, which are recognised by a monoclona antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis treatments. The peptides may also be used as vaccines against meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide(s) and corresp. antibodies for the treatment of meningitis - the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis
 Proteinase K reistant; Neisseria meningitidis; epitope; mapping; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 47; Fig 5/10; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sharma LR, Van Alstyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09509232-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitis related homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis opacity related protein
                                              N. meningitidis 608B peptide CS-857.
                                                                            22-DEC-1996
                                                                                                          AAW04912;
                                                                                                                                       AAW04912 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detecting and preventing meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHAR/) SHARMA L
(VALS/) VAN ALSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoassay; diagnosis; treatment; prophylactic; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; opacity related
                                                                                                                                                                                                                   135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                          46
                                                                                                                                                                                                                                                                                                                                         15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                                                                                                                                                                                                     6 AALIALPAAALAEGASGFYVQADAAH-----AKASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identified by matching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-147431/19
                                                                                                                                                                                                                                              LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 114
                                                                                                                                                                                                                                                                                                         IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARMA L R.
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0127499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-CA00516.
                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ū
                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponding MRHAS peptides.
                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                Score 138.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigenic
                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein POPM3; vaccine;
sequence; MRHAS; RV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                  .5e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                   48;
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Gaps

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 24
                                                                       26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9 describes the epitope mapping of the 22 kD N. meningitidis protein. Identification was accomplished using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
                                                                                                                                                                                                                                                                                  AAU38252 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection
                   Haselbeck R,
                                                                                                  21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                 WO200170955-A2.
                                                                                                                                                                                  Salmonella typhi.
                                                                                                                                                                                                  Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                              Salmonella typhi cellular proliferation protein #143.
                                                                                                                                                                                                                                                14-FEB-2002
                                                                                                                                                                                                                                                                  AAU38252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 84; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1995;
17-MAR-1995;
           Yamamoto RT,
                                                                                                                             21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09629412-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                       61 FAVDYTRYKNYKQVPSTDFKLYSIGA 86
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                              1 FAVDYTRYKNYK-APSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                      25 AA;
                                                     2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamel J,
           Xu HH;
                   Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0001983.
95US-0406362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-CA00157
                                                                                                                                                                                                                                                                                                                                                                          13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin D,
                  Zyskind JW,
                                                                                                                                                                                                                                                                                  257
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                 Score 118.5; DB 1
Pred. No. 8.7e-06;
0; Mismatches 1
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                   Wall D,
                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                  Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                  Length
                   Carr
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                 1;
 AAU34556
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
21-MAR-2000; 2000US-191078P
                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                E. coli cellular proliferation protein #137
                                                                                                                                    14-FEB-2002
                 21-MAR-2001; 2001WO-US09180.
                                                    WO200170955-A2
                                                                     Escherichia coli.
                                                                                                                                                                     AAU34556 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3;
                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                 201 VWYMDIDTTANYK-MGGVQQHDSVRLDPWVFMFSAGXR 237
                                                                                                                                                                                                                                   142 --- VDLDAGYRYNYIGKVNTVKNVRSGE----LSAGVR 172
                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                    VRPYVG--VGVNYTTFFDNDENDNGKKTGLSDLSFKDSXGAAGQVGVDYLINRDWLIGAS
                                                                                                                                                                                                                                                                      VKPYLGARLSLNRASV---DFNG-----SDSFSQTSTGLGVLAGVSYAVTPN-----
                                                                                                                                   (first entry)
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invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611495/70.
N-PSDB; AAS56111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                             1 MKKALAALIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
QLG-LTFTYMATDNIGVELLAATPFR-HKVGTGATGDIATVHLLPPTLMAQWYFGDSSSK 142
                                                                              RINDLREAVDYTRYKNYKQVPSTDFKLYSIGASAIYDF-----
                                                                                                                                                  MKKFTVAALALTILLSGSAFAHEAGEFFMRAGPATVRPTEGAGGTLGHLNGFD--VSNNT 84
                                                                                                                                                                                                                                                                                                                                               h 11.4%; Score 99.5; DB Similarity 25.2%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq ID No 13845; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 AA;
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                        81;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                               Length 257;
                                                                              ------DTQSP 97
                                                                                                                                                                                                                                                                                                        53;
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RESULT 10
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa aureus faccalis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at
             Non-typable Haemophilus influenza (NTHi) fimbrin protein.
                                                      09-AUG-1995
                                                                                                                           AAR66294 standard; Protein; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Seq ID No 10149; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotics, comprise sequences of antisense nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                           142 --- VDLDAGYRYNYIGKVNTVKNVRSGE----LSAGVR 172
                                                                                                                                                                                                                                                                                                                                 98 VKPYLGARLSLNRASVDFNG------SDSFSQTSTGLGVLAGVSYAVTPN-----
                                                                                                                                                                                                                                                                                                                                                                      59 QLG-LTFTYMATDNIGVELLAATPFR-HKIGTRATGDIATVHHLPPTLMAQWYFGDASSK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKLTVAALAVTTLLSGSAFAHEAGEFFMRAGSATVRPTEGAGGTLGSLGGFS--VTNNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALAALIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides for the identification and development of ibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                       VWYMDIDTTANYK-LGGAQQHDSVRLDPWVFMFSAGYR 211
                                                                                                                                                                                                                                                                                              FRPYVGA--GINYTTFEDNGFNDHGKEAGLSDLSLKDSWGAAGQVGVDYLINRDWLVNMS
                                                                                                                                                                                                                                                                                                                                                                                                         2001-611495/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-2536258
; 2000US-257931P.
; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%; Score 95.5; DB 24.8%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The fimbrin proteins from 15 randomly selected type b and non-typable clinical isolates of Haemophilus influenzae share common epitopes. Thus frimbrin isolated from non-typable Haemophilus influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause otitis media. Finbrin protein is produced by culturing a transformed microbial host, pref. E.coli, Sporodoptera frugiperda or a mucosal pathogen. Fimbrin protein (FP) produced by this process is claimed. The FP protech migrates in polyacrylamide genes to a posn. equiv. to a mol. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
            24-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9426304-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fimbrin protein; vaccine; otitis media.
                                            AAR96210;
                                                                         AAR96210 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-006359/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenza strain 1128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OHIO-) OHIO STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                    176
                                                                                                                                                                                                                116
                                                                                                                                                                                                                                              108
                                                                                                                                                                                 140 PNVDLDAGY-----RYNYIGKVNTVKNVRS--GELSAGVRVKF 175
                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                      54 YRINDLREAVDYTRYKNYKQVPSTDFKL----YSIGASAIYDFDTQSPVKPYLGARLS 107
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  1 MKKALAALIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG 53
                                                                                                                                                    PELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF
                                                                                                                                                                                                                LKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYAVL
                                                                                                                                                                                                                                             LNRASVDFNGSDSFSQTSTGL-----
                                                                                                                                                                                                                                                                           YRRNTFTYGV----FGGYQILNQDNFGLAAELGYHDFGRAKLREAGKPKAKHTNHGAYLS 115
                                                                                                                                                                                                                                                                                                                                     MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolattukudy PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9308-0065442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= amino terminus
                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                              10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 95.5; DB Pred. No. 0.092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sirakova
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                  ; 68
                                                                                                                                                                                                                                              ----GVLA-GVSYAVT 139
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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(first entry)

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                                                                                                                                                                                                              The sequence represents a fusion protein of a Yersinia
C enterocolitica attachment-invasion-locus (AII) protein (AAR96207)
CWith maltose binding protein (MBP, AAR96208). The MBP N-terminal
C portion of the fusion protein acts as an affinity tail, allowing
C efficient recombinant protein purification by amylose affinity
C chromatography. The receptor binding region of the AII protein
C chrowless all or some of the regions from the 4 extracellular loops.
C first region retains the binding affinity of the protein, and may be
C used alone or as part of a fusion protein for drug delivery. The
C bacterial AII protein may be complexed with a therapeutic agent to
C transport the agent across the gastrointestinal membrane barrier by
C transport the agent across the gastrointestinal membrane barrier by
C delivery system allows improved transport across enterocytes and
C gut or early release of biologically active material, and
                                                                                                                                Query Match
Best Local
                                                                                                                   Matches
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Therapeutic delivery system utilising bacterial invasin protein is not readily degraded in the gut, enhances systemic bio-availability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 15; 110pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-251447/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Habberfield AD,
                                                                                                                                                                                                         eliminates the need for parenteral administration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAY-1996.
                                               396 SVPGRGSIEGRASVNVY---AASESSISIGYAQSHVKENGYTLDNDPKGFN--LKYRYEL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09613250-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attachment-invasion-locus protein; maltose binding protein; fusion protein; affinity tail; amylose; affinity chromatogr purification; drug delivery; gastrointestinal membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIL protein-maltose binding protein fusion protein.
57 NDL-----REAVDYTRYKNY---KQVPSTDFKLYSIGASAIYDFDTQSPVKPYIGARLSL 108
                                                                                    12
                                                                                                                                ocal Similarity
                                                                            ALPAAALAEGASGFYVQADAAHAKASSSLGSA------KGFSPRISAGYRI 56
                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic;
                                                                                                                                                                             568 AA;
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bioavailability; enterocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ); affinity tail; amylose; affinity chromatography; delivery; gastrointestinal membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0331393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US13749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="reprise -_ 508..525 /note= reprise from extracellular loop-3" /note= reprise from extracellular loop-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "l
393..568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jensen-Pippo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464..482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425..440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterocolitica.
                                                                                                                              10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Peptide from extracellular loop-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Peptide from extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Maltose binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Attachment-invasion-locus protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                29;
                                                                                                                             Score 95.5; DB 17; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 χ,
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peyers patch M-cell
                                                                                                                71;
                                                                                                                                           Length 568;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loop-1"
                                                                                                           35;
                                                                                                           Gaps
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                                                                                                                                                                                                                      RESULT 12
AAP82053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                          Matches
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                      The protein is isolated from the OMP of P. aeruginosa serotype 6 ATTCC 3354) and purified by HPLC. The amino-terminal and trypsin fragments are sequenced and a series of oligonucleotide probes constructed corresponding to the established sequences. These probes used to screen a gene bank of 15-20 kb fragments of genomic DNA in lambda EMBL 3. One positive clone includes a 15 kb insert conty. the protein gene, which can be isolated as a 2.5 kb pstI fragment of the ground int a high copy no. vector because of the toxicity of the gene prod... so is subcloned as two fragments with an overlapping region of about 500bp. Ab's are raised by usual immunisation or cell-fusion procedures. The Ab's are useful in diagnosis.
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; ; p; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domdey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein F; OMPF; vaccination; antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein F of Pseudomonas aeruginosa.
104 ARLSLNRASVDENGSDSFSQTSTGLGVLAGVSYAVTPN----VDLDAGYRYNYIGKVNTV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New outer membrane protein F of Pseudomonas aeruginosa -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP82053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP82053 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 VKASV-FDESISASKTSMAYG--AGVQFNPLPNFVIDASYEYS---KLDSIK-VGTWMLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451
                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 AGYR 567
                                                                 50
                                                                                                                    1 MKKALAALIALALPAAAL---AEGASGFYYQA------DAAHAKASSSLGSAKGFSPR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences encoding it and
                              ----FLTDDVELALSYGEYHDVRGTYETGNKKVHGNLTSL--DAIYHFGTPGVGLRPYVS
                                                           ISAGYRINDLRFAVDYTRYKNYKQVPSTDFK-----LYSIGASAIYDFDTQS-PVKPYLG 103
                                                                                         LKNTLGVVIGSLVAASAMNAFAQGQNSVEIEAFGKRYFTDSVRNMKNADLYGGSIGY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDNWGVIGSFAYTHQGYDFFYGSNKFGHGDVDYYSVTMGPSFRINEYVSLYGLLGAAHGK 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGVR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRASYDFNGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN82023
                                                                                                                                                                                                                    350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lottspeich F,
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87DE-3718591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis.
                                                                                                                                                                       10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Von
                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AA
                                                                                                                                                                  Score 93.5; DB Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived antibodies, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Specht B-U, Duchene
                                                                                                                                                       Mismatches
                                                                                                                                                                                 DB 9; Length 350;
                                                                                                                                                      82;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X
                                                                                                                                                    37;
                                                                                                                                                  Gaps
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RESULT 13
AAB59179
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Best Local S
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                               The present invention relates to a Campylobacter jejuni or Campylobacter coli fibronectin binding protein (CadF). A recombinant expression vector with cadF is useful in an assay for determining the presence of C.jejuni or C.coli in a test sample or for determining whether a test isolate of Campylobacter is a strain of C.coli. cadF is useful in the construction of DNA probes for identifying and quantifying the level of expression of CadF in a cell. The gene can also be used in a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polynucleotide useful for producing fibronectin binding proteins which are useful in production of vaccine, in diagnostic assays and for prophylactic and therapeutic purposes .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibronectin binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein associated with C.coli and C.jejuni CadF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB59179 standard; protein; 350 AA
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 37-40; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-079546/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 DNGHQGEWMAGLGVGF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 KNVRSGELSAGVRVKF 175
                                                            114
 167
                                                                                       104 ARLSLNRASVDFNGSDSFSQTSTGLGVLAGVSYAVTPN----VDLDAGYRYNYIGKVNTV 159
                                                                                                                        60
                                                                                                                                                    50
                                                                                                                                                                                  w
                                                                                                                                                                                                               1 MKKALAALIALALPAAAL---AEGASGFYVQA-----DAAHAKASSSLGSAKGFSPR 49
                                                                                                                      ----FLTDDVELALSYGEYHDVRGTYETGNKKVHGNLTSL--DAIYHFGTPGVGLRPYVS 113
                                                                                                                                                                                  LKNTLGVVIGSLVAASAMNAFAQGQNSVEIEAFGKRYFTDSVRNMKNADLYGGSIGY--- 59
 DNGHQGEWMAGLGVGF 182
                          KNVRSGELSAGVRVKF 175
                                                                                                                                                   ISAGYRINDLRFAVDYTRYKNYKQVPSTDFK-----LYSIGASAIYDFDTQS-PVKPYLG 103
                                                          AGLA-HONITNINSDSQGRQQMTMANIGAGLKYYFTENFFAKASLDGQY-----GLEKR 166
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                        350 AA;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Konkel ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0046763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0080025
                                                                                                                                                                                                                                                           10.7%; Score 93.5; DB 23.5%; Pred. No. 0.15;
                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CadF; vaccine; diagnostic assay.
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                          Length 350;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                               9;
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Matches
          Best Local Similarity
                     Query Match
                                                                     This sequence represents the major outer membrane protein P5 of non-typeable H. influenzae. One or more surface exposed loops of this protein may be replaced with a modified peptide of the invention. Each of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP P5 from strain ntHill28, representing amino acids Arg117 to Gly135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP P5 may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB47447 standard; Protein; 353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB47447;
                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOMP P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200161013-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                         Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                otitis media and conjunctivitis -
                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                         Berthet FJ, Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000; 2000GB-0003502
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001; 2001WO-EP01556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2001.
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                  2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory tract infection.
                                                 353
Conservative
                                                 Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Extracellular domain"
89..100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 38..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Loop
            10.7%; Score 93.5; DB 24.9%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150
                                                                                                                                                                                                                                                                                                                                                                          Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lоор 4
 29;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Thonnard
                          DB
                         22;
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 89;
 Indels
                         Length 353;
 45;
 Gaps
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AAB44589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                         Matches
                                                                                        Query Match
Best Local
                                                                                                                                                                        The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                           Claim 39; Pages 308-309; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                       Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                     wound infections.
                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAC79664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowery DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000; 2000WO-US09218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200061724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virulence gene protein #69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB44589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB44589 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 YQWLTRYGKYRPQDKPNTALNYNPWIGSINAGISYRF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 Y----RYNYIGKVNTVKNVRS--GELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LDVYGKAGVALVRS--DYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 VKPYLGARLSLNRASVDFNGSDSFSQTSTGLG-----VLAGVSYAVTPNVDLDAG 147
1 MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                              1 MKKALAALIALALPAAALAEGA---SGFYVQADAAHAKASSSLGSAK-GFSPRI---SAG 53
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YGVFGGYQILNQNNLGLAVELGYDDFGRAKG-REKGKTVVKHTNHGTHLSLKGSYEVLEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 PRISAGYRI---NDLRFAV-----DYTRYKNYKQVPSTDFKLYSIGA--SAIYDFDTQSP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTAIALYVAGLAAASVAQAAPQENTFYAGVKAGQASFHDGLRALAREYKVGYHRNSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                               2000-647422/62.
                                                                                                                                    369 AA;
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                                                                     Conservative
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99US-0153453.
                                                                10.7%; Score 93.5; DB 21; 23.2%; Pred. No. 0.16; tive 34; Mismatches 78;
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174 ILP--ELAARVEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRF 224
                                           138 VTPNVDLDAGYRYNYIGKVNTVKN--VRSG------ELSAGVRVKF 175
                                                                                     114 NLALKPSYEVLPDLDVYGKVGIAVVRNDYKKYGAENTNESTTKFHKLKASTILGAGVEYA 173
                                                                                                                               95 QSPVKP-----YLGARLSLNRASVDFNGSDSFSQTSTGLGVL-----AGVSYA 137
                                                                                                                                                                        59 YGIN--RNSVTYGVFGGYQILNQNNF---GLAAELGYDYYGRVRGNVDEFRTVKHSAHGL 113
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Search completed: October 28, Job time: 26.8565 secs 2002, 16:00:38

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                and is derived by analysis of the total score distribution.
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874
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Gapop 10.0 , Gapext 0.5
                1 MKKALAALIALALPAAALAE......VNTVKNVRSGELSAGVRVKF 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-913-362-4
US-08-913-362-30
US-08-913-362-8
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US-08-913-362-8
US-08-913-362-26
PCT-US-91-362-26
PCT-US-91-362-26
PCT-US-91-32-26-6
US-08-467-722A-2
US-08-467-722A-2
US-08-382-184-3
US-08-382-184-3
US-08-382-184-3
US-09-132-528-4
US-08-382-184-3
US-09-132-528-2
US-08-641-356-3
US-08-382-184-2
US-08-382-184-2
US-08-641-356-2
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US-09-132-528-3
US-08-818-111-53
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637	867	897	613	448	483	474	478	337	478	487	990	913	883	913	896	056	056
-65	-92	-43	-00	-19	-57	-67	-37	-48	IS-08-478-435-94	-89	-16	-36	-51	-36	-68	-09-056-556-21	-09-056-556-53
4-9	1-4	9-8	9A-	4-4	7A-	1-9	3-9	3-9	5-9	0A-	7-2	2-1	5-2	2-2	5A-	6-2	5-5
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ALIGNMENTS

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RESULT 1
US-08-913-362-4
; MOLECULE TYPE: US-08-913-362-4
                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION
REGISTRATION NUMBER: 29,768
REGENERATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08913362 Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Brodeu
                                                                                                TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TELEX: 404132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAIL.
COUNTRY: USA
ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley (
STREET: 3000 K Str
CITY: Washington
STATE: D.C.
                                         TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                LENGTH:
                                                           amino acid
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3000 K Street, N.W.,
                                                                                    175 amino acids
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Rioux, Clement
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Query Match

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Score 874;

DB 4;

Length 175;

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US-08-913-362-30
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                                                                       Matches
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; Pred. No. 4e-92; Matches 175; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
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                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                           TYPE: amino acid
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                                                                                    Match 96.5%;
Local Similarity 96.6%;
                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                              TELEPHONE:
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20007-5109
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3000 K Street, N.W., Suite 500
                                                                     Conservative
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(202)672-5399
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                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                047998/0128
                                                                     0; Mismatches
                                                                  Score 843; DB 4; Length 175; Pred. No. 1.4e-88; 0; Mismatches 6; Indels
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Qy	Оy	ДУ	Query Best Matcl	Db US-08-	Qy	Ωу
121 FSQTSTGLGVLAGVSYAVTÞNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175	61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120 	1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60 	Query Match 95.9%; Score 838.5; DB 4; Length 174; Best Local Similarity 97.1%; Pred. No. 4.5e-88; Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;	121 FSQTSXGJGVLAGVSYAVTFNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 913-362-6 ence 6, Application US/08913362 mt No. 6287574 ERAL INFORMATION: PPLICANT: Brodeur, Bernard R PPLICANT: Martin, Denis PPLICANT: Riburton: OF NEISSERIA MENINGITIDIS ORRESSED: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STRATE: D.C. COUNTRY: USA COUNTRY: USA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION DATA: APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995 TRICA PPLICATION DATA: APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995 TORNEY/AGENT INFORMATION: APPLICATION NUMBER: US 00/001,983 FILING DATE: 10-AUG-1995 TORNEY/AGENT INFORMATION: APPLICATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 29,768	121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175	61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120

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FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174

GENERAL INFORMATION:

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US-08-913-362-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 047998/0128 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
                                                                                                   120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                     121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGYRVKF 175
                                                                                                                                                                                       61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
                                                                                                                                                                     61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                        1 MKKALATLIALAPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                            1 MKKALAALIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (202)672-5300
(202)672-5399
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Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                               94.3%;
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                                                                                                                                                                                                                                                                                                            Score 824.5; DB 4; Length 174; Pred. No. 1.8e-86; 0; Mismatches 7; Indels 1
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RESULT 6
US-08-127-499A-20
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                                                                                                      Sequence 20, Application US/08127499A Patent No. 5510264 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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              APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARWA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
 CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                           120 FSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                          121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGYRVKF 175
                                                                                                                                                                                                                                                                                              61 FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDS
                                                                                                                                                                                                                                                                                                                 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSDVKPYLGARLSLNRASVDFNGSDS 120
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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Rioux, Clement
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ADDRESS
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04-AUG-1995
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93.7%;
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Pred. No. 3.2e-85;
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US-08-482-847-20
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Best Local Similarity
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Patent No. 5556757
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                     APPLICANT: VAN ALSTYNE, Diane APPLICANT: SHARMA, Lawrence Rejendra TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGTITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                          ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
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APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
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3000 K Street, N.W., Suite 500
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                                                                                                                                                                                  USA
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                   US/08/482,847
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
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PRIOR APPLICATION DATA:
                                                                                      APPLICATION NUMBER: US/08/913,362
FILLING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
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CITY: Washington
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                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Hamel, Josee
Rioux, Clement
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202)672-5300
(202)672-5399
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                                                                         US 60/001,983
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US-08-913-362-26
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GENERAL INFORMATION:
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Best Local Similarity 92.3%;
Matches 24; Conservative
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SEQUENCE CHARACTERISTICS
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Neisseria m STRAIN: 608B
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TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
511 VKASV-FDESISASKTSMAYG--AGVQFNPLPNFVIDASYEYS---KLDSIK-VGTWMLG 563
                      109 NRASVDFNGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYLGKVNTVKNVRSGELS 168
                                                                                                                                         396 SVPGRGSIEGRASVNVY---AASESSISIGYAQSHVKENGYTLDNDPKGEN--LKYRYEL 450
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LENGTH: 25 amino acids
                                                                     451 DDNWGVIGSFAYTHQGYDFFYGSNKFGHGDVDYYSVTMGPSFRINEYVSLYGLLGAAHGK 510
                                                                                                     57 NDL----RFAVDYTRYKNY---KQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSL 108
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                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/13749
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California
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                                                                                                                                                                                                                                                                                                                                                                                568 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amgen Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                10.9%; Score 95.5; DB 5; Length 568; 26.6%; Pred. No. 0.019; tive 29; Mismatches 71; Indels 3
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Pred. No. 4.2e-07;
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: Sequence 2, Application US/08467722A
: Patent No. 6030626
: GENERAL INFORMATION:
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; MOLECULE TYPE: protein
US-08-457-997B-2
                                                                                RESULT 11
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US-08-457-997B-2
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NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,8
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LENGTH: 359 amino acid
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APPLICATION NUMBER: US
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                                                                                                                              171 EYAVLPELAVRLEYQWLTRYGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                                                                                                                                                                                       111 GAYLSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGA 170
                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                      135 SYAVTPNVDLDAGY-----RYNYIGKVNTVKNVRS--GELSAGVRVKF 175
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                                                                                                                                                                                                                                                                                 60 YRRNTFTYGY----FGGYQILNQDNF-----GLAAELGYDDFGRAKLREAGKPKAKHTNH 110
                                                                                                                                                                                                                                                                                                                     54 YRINDLRFAYDYTRYKNYKQVPSTDFKLYSIGASAIYDFD-----TQSPVKPYL---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                           1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      h 10.7%; Score 93.5; DB Similarity 23.5%; Pred. No. 0.017; 54; Conservative 29; Mismatches
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amino acid
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Suite 1800 800 Superior Avenue
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Kolattul TITLE OF INVENTION:

Kolattukudy, P. E. VENTION: Otitis Media Vaccine

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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-733-230-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (216) 622-8458; TELEFAX: (216) 241-0816; INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 359 amin
                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08733230 Patent No. 6025338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Barbet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                              APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
                                                                                                                                                                                                                                  APPLICANT: Ganta, Roman Reddy
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael
                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                             TITLE OF INVENTION: Nucleic Acid Vaccines Against TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 EYAVLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 SYAVTPNVDLDAGY-----RYNYIGKVNTVKNVRS--GELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GAYLSLKGSYEVLDGLDYYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 5--
CTTY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 GARLSLNRASVDFNGSDSFSQTSTGL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 YRINDLRFAYDYTRYKNYKQVPSTDFKLYSIGASAIYDFD-----TQSPVKPYL----- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Match 10.7%; Score 93.5; DB 3; Length 359; Local Similarity 23.5%; Pred. No. 0.017; Local Similarity 23.5% Pred. No. 82; Indels 6 685 54; Conservative 29; Mismatches 82; Indels 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                 ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
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44114-2688
Gainesville
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                                                                                                                                                                                                                                  McGuire, Travis C.
Burridge, Michael J.
                                                                                                                                                                                                                                                                                                     Barbet, Anthony F
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Matches
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                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acid
                                                                          CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McGuire, Travis C. APPLICANT: Burridge, Michael
                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans FILE REFERENCE: UF-167Cl
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barbet, Anthony APPLICANT: Ganta, Roman R.
                                                                                                                                                                                                                                                                                        APPLICANT: Rurangirwa, Fred R. APPLICANT: Mahan, Suman M.
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TYPE: PRT
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                   LENGTH: 282
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 ASVK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 ---KQVTTKLAYRGKVGISYQFTPEISLVAGGFYHGLFDESYKDIPAHNSVK--FSGEAK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 DSFSQTSTGLGV--LAGVSYAVTPNVDLDAG-----YRYNYIGKVNTVKNVRSGELS 168
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Nyika, Aceme
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                                                                                                                                                                                                                                                                                                                                                                                                                     Anthony F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.8%; Score 86; DB 3; Length 282; 26.6%; Pred. No. 0.083;
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                                                                                                                       Query Match
Best Local 9
                                                                                      Matches
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Best Local Similarity
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/382,184
                                                                                                                                                                                                                                                  MOLECULE TYPE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acid
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NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Anaplasma marginale
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TITLE OF INVENTION:
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10 ALALPAAALAEGASGFYVQADAAHAKASSSLGSA-----KGFSPRISAGYRINDLRFA 62
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FILING DATE: 01-FE
CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1755 S. CITY: Arlington STATE: Virginia
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                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                               43;
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                                                                                                                                                                                                                                                                                      peptide
                                                                                              9.8%; Score 86; DB 1; Length 286; 27.9%; Pred. No. 0.085;
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MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
AND FOR THE DETECTION OF TUBERCULOSIS
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26.6%; Pred. No. 0.083;
tive 17; Mismatches
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Best Local Similarity
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
120 -----SFSQTSTGLG-VLAGVSYAVTPNVDLDAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                  128 LGRLDQKLYASAEATDSK-----AAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                    63 VDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSD--- 119
                                                                                                                                                            10 ALALPAAALAEGASGFYVQADAAHAKASSSLGSA------KGFSPRISAGYRINDLRFA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Pelance ""
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                                                                                                                         82 SFALPAG-----WVESDAAHFDYGSALLSKTTGDPPFPGQPPPVA-----NDTRIV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OBLON, NORMAN F
REGISTRATION NUMBER:
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ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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27.9%; Pred. No. 0.085;
ative 15; Mismatches
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MICRODROANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
AND FOR THE DETECTION OF TUBERCULOSIS
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Db 183 SYYEVKFSDPSKPNGQIWTGVIGSPAANAP-DAG 215

Search completed: October 28, 2002, 16:04:19 Job time: 10.5409 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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       US-09-684-883-4
874
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ALIGNMENTS

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 sero C;Species: Neisseria meningitidis C;Decies: Neisseria meningitidis C;Date: 05-NAY-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: B81932

R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Hollroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491 A;Reference number: A81775; MUID:20222556 A;Accession: B81932

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-174 < PAR>

A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84143.1; PID:g737A;Experimental source: serogroup A, strain Z2491

A; Gene: nspA; NMA0862

Ş Matches 170; Query Match Local Similarity Conservative 95.9%; 97.1%; 0, Score 838.5; DB 2; Pred. No. 3.2e-66; Mismatches 4; Indels Length 174; 1; Gaps ۲,

δÃ 밁 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60 1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60

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61

В 120 121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGYRVKF 175 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174

FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS

RESULT 2 G81174

Outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: G81174
R;Tettelin, H; Saunders, N.J; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Oin, H; Vamathevan, J; Gill, J; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Ithle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755 A;Accession: G81174 A;Status: preliminary

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C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
C;Accession: S16611; S36345; S28624
R;Bhat, K.S.; Gibbs, C.D.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
A,Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam: A;Reference number: S16610; MUID:92114767
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A;Residues: 1-174 <TET>
A;Residues: 1-174 <TET>
A;Cross-references: GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAF41081.1; PID:g722588
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                                                                                                                                                                                      F;75-83/Domain: transmembrane #status predicted <TM2>F;88-94/Domain: transmembrane #status predicted <TM3>F;88-94/Domain: transmembrane #status predicted <EXT2>F;95-133/Domain: extracellular #status predicted <TM4>F;101-128/Region: hypervariable region HV1
F;134-148/Domain: transmembrane #status predicted <TM4>F;134-148/Domain: transmembra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: opacity protein
C; Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 24-260 <KUP>
A;Cross-references: EMBL:Z18937; NID:g49333; PIDN:CAA79370.1; PID:g940799
A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of tran
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Variable opacity (Opa) outer membrane proteins account for the A; Reference number: $36328; MUID:93178439
A; Accession: $36345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X52371
A;Experimental source: strain MS11, variant 4.8
A;Experimental source: strain MS11, variant 4.8
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat
A;Note: expression of opacity proteins is regulated by the number of translated repeat
Of repeats place the start codon in frame with the rest of the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-260 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                           F;43-74/Domain: extracellular #status predicted <EXT1>F;51-60/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;24-260/Product: opacity protein opaJ #status predicted F;34-42/Domain: transmembrane #status predicted <TML>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
F;165-211/Domain: extracellular *status
F;170-217/Region: hypervariable region F
F;212-224/Domain: transmembrane *status
                                                                                                                                                 F;154-164/Domain: transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 госат
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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96.0%;
                                         #status predicted region HV2
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     predicted <TM6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the authors did not translate the sequence for the signal peptide A;Note: expression of opacity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opacity protein opaK precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N;Alternate names: outer membrane protein opaK
                                                                                                                                                                                                                                                                                F;76-84/Domain: transmembrane #status predicted <TM2>
F;89-95/Domain: transmembrane #status predicted <TM3>
F;96-134/Domain: extracellular #status predicted <EXT2>
                                                                                                                                                                                                                                                                                                                                                                                                          F;1-10,11-23/Domain: signal sequence (fragments) #status F;24-261/Product: opacity protein opaK #status predicted F;34-42/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: x52364
A; Experimental source: strain MS11, variant 4.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                           F;171-218/Region: hypervariable F;213-225/Domain: transmembrane
                                                                                                                                                                                                          F;135-149/Domain: transmembrane F;155-165/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                               F;51-61/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                      F;43-75/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
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                                                                                                                    F;229-237/Domain: transmembrane
                                                                                                                                                                                                                                                               F;102-129/Region: hypervariable region HV1
                                                                                                                                                                                           F;166-212/Domain: extracellular
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 KNVRSGELSAGVRVKF 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKALAALIALALPAAALAEG---ASGFYVQADAAHA-----KASSSLGSAKGFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opaK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R-FKTHEASLGVRYRF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPGTTPTVYPGKNTQDAHRESDSIRRVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NGSDSFSQTST----GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PRISAGYRINDLRFAVDYTRYKNY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVDF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                        extracellular #status predicted <EXTl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                      transmembrane
                                                                                                extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                      #status
                                                                                                                                                                    #status predicted <EXT3> region HV2
                                                                                                                                                                                                                    #status predicted
                                                                                                                                                                                                                                           #status predicted <TM4>
                                                                                                                      #status predicted
                                                                                                #status
                                                                                                                                           #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
  Score
Pred.
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  242; DB 2;
No. 7.6e-14;
                                                                      predicted
                                                                                             predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                <1M6>
                                                                                                                           <TM7>
                                                                                                                                                                                                                         <TM5>
                      Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translated repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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Local Similarity 28.7%; Pred. No. 9.2e-14; 28.7%; Pred. No. 9.2e-14; 28.7%; Pred. No. 9.2e-14; 28.7%; Pred. No. 9.2e-14; 29.7%; Conservative 26; Mismatches 69; Indels 10. ALALPAAALAEGASGFYVQADAAHAKASSSIGSAKG	F;176-186/Domain: transmembrane #status predicted <tm5> F;187-234/Domain: extracellular #status predicted <ext3> F;192-240/Region: hypervariable region HV2 F;192-240/Region: transmembrane #status predicted <tm6> F;251-247/Domain: transmembrane #status predicted <tm6> F;251-259/Domain: transmembrane #status predicted <tm7> F;251-259/Domain: extracellular #status predicted <ext4> F;250-244/Domain: transmembrane #status predicted <tm8> F;275-283/Domain: transmembrane #status predicted <tm8> Ouerv Match 27.6%: Score 241 5: DR 2: Tength 283.</tm8></tm8></ext4></tm7></tm6></tm6></ext3></tm5>	F:1-48/Domain: signal sequence #status predicted <sig> F:49-283/Product: opacity protein opaH #status predicted <mat> F:58-66/Domain: transmembrane #status predicted <fmi> F:67-98/Domain: extracellular #status predicted <fmi> F:75-84/Region: semivariable region F:99-107/Domain: transmembrane #status predicted <tm2> F:112-118/Domain: transmembrane #status predicted <tm3> F:119-155/Domain: extracellular #status predicted <fm3> F:119-155/Domain: hypervariable region HV1 F:156-170/Domain: transmembrane #status predicted <fm4></fm4></fm3></tm3></tm2></fmi></fmi></mat></sig>	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-283 <wall> A;Cross-references: EMBL:U13708; NID:g535357; PIDN:AAA74082.1; PID:g535358 A;Experimental source: isolate 15063g A;Experimental source: isolate sequence was submitted to the EMBL Data Library, August 1994 A;Note: the nucleotide sequence was submitted by the number of translated repeat e Of repeats place the start codon in frame with the rest of the protein C;Superfamily: opacity protein</wall>	RESULT 5 \$72343 \$72343 \$72343 \$72343 \$7343 \$7344 \$7344 \$7344 \$7344 \$7344 \$7344 \$7344 \$7344 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346 \$7346	Db 141 LGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNT 200 Qy 119DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRV 173	Matches 75; Conservative 24; Mismatches 61; Indels 82; Gaps 10; Qy 15 AAALAEG-ASGFYVQADAAHAKASSSLGSAKGFSPRI 50
Qy 45GFSPRISAGYRINDLE	Query Match 27.5%; Best Local Similarity 28.3%; Matches 72; Conservative 2 KKALAALIALALPAAALAEG 6 KKPSLLFSSLLFSSAAQAAGEE	F;90-131/Domain: extracellular #st F;90-131/Domain: extracellular #st F;101-125/Region: hypervariable re F;132-146/Domain: transmembrane #s F;152-162/Domain: extracellular #s F;163-209/Domain: extracellular #s F;168-215/Region: hypervariable re F;210-222/Domain: transmembrane #s F;226-234/Domain: transmembrane #s F;235-249/Domain: extracellular #s F;230-258/Domain: transmembrane #s	rity protein riface components signal sepacity protein samembrane tracellular nivariable unsmembrane	C;Accession: Sibbiz R;Bhat, K.S.; Gibbs, C.P.; Barrera Mol. Microbiol. 5, 1889-1901, 1991 A;Fitle: The opacity proteins of N A;Reference number: S16610; MUID:9 A;Accession: S16612 A;Accession: S16612 A;Molecule type: DNA A;Residues: 1-258 <bha> A;Cross-references: EMBL:X52369 A;Cross-references: EMBL:X52369 A;Experimental source: strain MS:1 A;Note: the authors did not transl A;Note: expression of opacity proto of repeats place the start codon i C;Genetics:</bha>	Juste Ya	101 PH 83 SI .161 SI 118

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#status predicted <TM2>
#status predicted <TM3>
#status predicted <EXT2>
#status predicted <TM4>
#status predicted <TM4>
#status predicted <TM5>
#status predicted <TM75>
#status predicted <TM73>
#status predicted <TM79>
#status predicted <TM79>
#status predicted <TM79>
#status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nt; transmembrane protein
ence (fragments) #status predicted <SIG>
n opaE #status predicted <MAT>
tatus predicted <TMI>
tatus predicted <EXTI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11, variant 4.8 slate the sequence for the signal peptide oteins is regulated by the number of translated repea in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                 Score 240.5; DB 2; Length 258;
Pred. No. 1e-13;
28; Mismatches 73; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ra, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 171
| :|| :|| ||||:| |: : :| | |:
VGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGM 279
                                 TQSPVKPYLGARLSLN--RASVDF------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVAYGHVRHSIDSTKKTTKILTSFYGVATKPTTYDIGP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLSLN--RASVD------FNG------ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWNNNKYSVNIERVQEAHSNRIDLKAENQENGTFHAVS 160
NDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGP 185
                                                                                                VRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                  HGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 65
                                                                                                                                                                                                                                                  -ASGFYVQADAAHA-----KASSSLGSAK----- 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae strain MS11 are encoded by a f:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ision 17-Oct-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrhoeae (strain MS11) (fragments)
                                                                                                                                                                                                                                                                                                 73; Indels 81;
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                 8
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RESULT 8
S16613
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F;142-188/Domain: extracellular #status predicted <EXT3>
F:147-194/Region: hypervariable region HV2
F:189-201/Domain: transmembrane #status predicted <TM6>
F:205-213/Domain: transmembrane #status predicted <TM7>
F:214-228/Domain: extracellular #status predicted <EXT4>
F:229-237/Domain: transmembrane #status predicted <EXT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-237/Product: opacity protein opa57 #status predicted <MAT>
F;11-19/Domain: transmembrane #status predicted <TMI>
F;20-51/Domain: extracellular #status predicted <EXTI>
F;28-37/Region: semivariable region
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F;65-71/Domain: transmembrane #status predicted <TM3>
F;72-110/Domain: extracellular #status predicted <TM72>
F;78-105/Region: hypervariable region HV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-237 < KUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di A; Reference number: S36328; MUID:93178439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment) N;Alternate names: outer membrane protein opa57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         맑
opacity protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: opa57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z18935; NID:g49331; PIDN:CAA79368.1; PID:g940797
A;Experimental source: strain MS11, variant F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S36343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ЕМВО J. 12, 641-650, 1993
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                                                                                                                        181
                                                                                                                                            122 SQTST----GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 VRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 GTTPTVYPGKNTQDAHRESDSIRRVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR- 244
                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ALAEGASGFYVQADAAHA------KASSSLGS-----AKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                               DFGGWRIAADYARYRKWNNNKYSVSIKELLRNKGNGNRTDLKAENQENGTFHAVSSLGLS 120
                                                                                                                                                                                                                                                                                                                                                              RINDLREAVDYTRYK - - - NYKQVPS - - - -
                                                                                                                                                                                                                                                                  AIYDFDTQSPVKPYLGARLSLN--RASVDF-----NGSDSF 121
                                                                                                                                                                                                                                                                                                                                                                                                              ASEDGGRGPYVQADLAYAYEHITHDYPEPTAPNKNKISTVSDYFRNIRTRSVHPRVSVGY 60
                                                                                                                                                                                                                  AVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNTQDAH 180
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                                                                                                                   RESDSIRRYGLGAVAGYGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
opaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
Neisseria gonorrhoeae (strain MS11) (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
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                                                                                                                                                                                                                                                                                                                                                              2; Length 237;
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                                             C; Accession: S20043
                                                              C;Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 17-Oct-1997
                                                                                          A; Variety: strain FAM18
                                                                                                                                                                                         S20043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene:
                    R; Aho,
Microbiol.
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G;Superfamily: opacity protein
G;Keywords: cell surface component; transmembrane protein
G;Keywords: signal sequence (fragments) #status
F;1-13,14-104/Domain: signal sequence (fragments) #status
opacity protein B precursor (clone pFLOB1700) - N;Alternate names: outer membrane protein class C;Species: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;224-289/Domain:
F;233-243/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded
A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Accession: S16613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;176-212/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;169-175/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;124-155/Domain:
F;132-141/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of repeats place the start codon in frame with the rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the authors did not translate the sequence for the signal peptide A; Note: expression of opacity proteins is regulated by the number of tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-338 <BHA>
A; Cross-references: EMBL: X52373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;330-338/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;290-302/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;213-227/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;182-207/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;156-164/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;115-123/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain MS11, variant 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S16613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                           336 YRF 338
                                                                                                                                                                                                   173 VKF 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                   GSDSFSQTST----GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVR 172
                                                                                                                                                                                                                                            TQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVR
                                                                                                                                                                                                                                                                                                                                                                        YSIGASAIYDFDTQSPVKPYLGARLSLN--RASVDF--------
                                                                                                                                                                                                                                                                                                                                                                                                                   HPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTENQENGTFHAV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPRISAGYRINDLRFAVDYTRYKNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLFAARAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKDKKSTVSDYFRNIRTHSI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status predicted
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28.8%;
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                                             Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <EXT3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <EXT2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 338;
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                                             (strain
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Dempsey, J.A.; H bl. 5, 1429-1437,

ноbbs, 17, 1991

M.M.; Klapper, D.G.; Cannon,

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RESULT 10
S16614
                                                                                                                                                                                                                                                                          A:Variety: strain MS11
C;Date: 04-Unn-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Accession: S16614
                                                                                                                                           R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam. A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-19/Domain: signal sequence (fragment) #status predicted <SIG>F;20-254/Product: opacity protein opaB #status predicted <MAT>F;40-69/Domain: transmembrane #status predicted <MAT>F;48-55/Domain: extracellular #status predicted <MAT>F;48-55/Domain: extracellular #status predicted <murt
                                  A; Molecule type: DNA
A; Residues: 1-257 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                     opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
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F:206-218/Domain: transmembrane #status predicted <TM6>F:222-230/Domain: transmembrane #status predicted <TM7>F:231-45/Domain: extracellular #status predicted <EXT4>F:231-45/Domain: extracellular #status predicted <EXT4
A;Cross-references: EMBL:X52368
                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Neisseria gonorrhoeae
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A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A; Note: only a part of the translation is shown
A; Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
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A;Accession: S20043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 STQNAYHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 SLGLSAIYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVVTLTHGGADTKPTIYNGE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 RVKF 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----FNGS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFSSAAQAASEDGSRSPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.4%;
28.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 239.5;
Pred. No. 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KQVPSTDFKLY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
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A; Note: 241 Val was also found
A; Note: expression of opacity proteins is regulated by the number of translated of repeats place the start codon in frame with the rest of the protein R; Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
                                                                                                                                                                                                           A;Reference number: S03095; MUID:89096501
A;Accession: S03095
A;MOleonle ****
                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-268 < VAN>
                                                                                                                                                                                                                                                                                                          R; van der Ley, P. Mol. Microbiol. 2
                                                                                                                  A; Experimental source: strain JS3
                                                                                                                                                 A; Cross-references: EMBL: X12625
                                                                                                                                                                                                                                                                                                                                                               C; Accession: 803095; 816360
                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Neisseria gonorrhoeae A; Variety: strain JS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      opacity protein P.IIc precursor - Neisseria gonorrhoeae (strain JS3) (fragments) N;Alternate names: outer membrane protein P.IIc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KONH2C
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F;209-221/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;75-83/Domain: transmembrane #status predicted <TM2>
F;88-94/Domain: transmembrane #status predicted <TM3>
F;95-131/Domain: extracellular #status predicted <EXT2>
F;101-126/Region: hypervariable region HVI
F;132-146/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Keywords: cell surface component; transmembrane protein F;1-10,11-23/Domain: signal sequence (fragments) #status | F;24-257/Product: opacity protein opaF #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Experimental source: strain MS11, variant 4.8
A:Note: the authors translated the codon ACC for residue 206 as Ala and TAT for resid A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repea
Of repeats place the start codon in frame with the rest of the protein
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F;225-233/Domain: transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;249-257/Domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F; 234-248/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: opacity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 LNPTVYTEENTQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-F 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 KTHEASLGVRYRF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 RSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKALAALIALALPAAALAEG---ASGFYVQADAAHA-----KASSSLGSAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NGSDSFSQTST----GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVDF--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GFSPRISAGYRINDLRFAVDYTRYKNY--------------
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                                                                                                                                                                                                                                                                                                             2, 797-806, 1988
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28.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 239; DB 2,
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                                                                                                                                                                                                                                                                   II-encoding sequence in the genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <EXT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 257;
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                                                                                                                                                                                                                                                                      of Neiss
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F;95-140/Domain: extracellular #status predicted <EXT2>F;101-135/Region: hypervariable region HVI
F;141-155/Domain: transmembrane #status predicted <TM4>F;141-155/Domain: transmembrane #status predicted <TM5>F;161-171/Domain: transmembrane #status predicted <EXT3>F;172-219/Domain: extracellular #status predicted <EXT3>
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A; Accession: $16360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
S36350
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F;51-60/Region: semivariable region
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 55, 2026-2031, 1987
A; Title: Antigenic and structural differences among six proteins II expressed by a sing
                                                                                                                                                                                                                                                                                                                                                                                                             opacity protein opa67 - Neisseria gonorrhoeae (strain VP1) (fragment) N;Alternate names: outer membrane protein opa67 C;Species: Neisseria gonorrhoeae
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                                                                                                                                                                                                                                                                                                                      A;Variety: strain VP1
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C;Accession: S36350; S28625
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                                                                                                                                                                                                                                      EMBO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
                                                                                                                                                                                                                                                                                        R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F
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A;Cross-references: EMBL:218942; NID:g49338; PIDN:CAA79375.1; PID:g940804
A;Experimental source: strain VP1
A;Experimental source: strain VP1
a;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                        A; Reference number: $36328;
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-233 < KUP>
                                                                                                                                                                               A; Accession: S36350
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Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TEHQENGTFHAVSSLGLSTIYDFDTGSRFKPYIGMRVAYGHVRHQVRSVEQETEIITTYP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 VKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 FNGSDSFSQTS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 -GFSPRISAGYRINDLRFAVDYTRYKNYK--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AALIALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAK----------- 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TR-FKTHEASLGMRYRF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---QVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRA-----SVD------ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSVHPRVSVGYDFGSWRIAADYARYRKWNNNKYSVSIKELLRNDNSASGVRGHLNIQTQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSLLFSSAARAASEDGGRGPYVQADLAYAAERITHDYPKPTGTGKNKISTVSDYFRNIRT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 239; DB 1; 27.2%; Pred. No. 1.4e-13;
                                                                                                                                                                                                                    MUID: 93178439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1'M3>
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88
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C;Genetics:
A;Gene: opa67
A;Gene: opa67
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-233/Product: opacity protein opa67 #status predicted <
F;1-193/Domain: transmembrane #status predicted <TM1>
F;11-19/Domain: extracellular #status predicted <EXT1>
F;20-52/Domain: extracellular #status predicted <EXT1>
F;38-38/Region: semivariable region
F;53-61/Domain: transmembrane #status predicted <TM3>
F:66-72/Domain: transmembrane #status predicted <EXT3>
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F;185-197/Domain: transmembrane #status predicted <TM5>F;201-209/Domain: transmembrane #status predicted <TM7>F;210-224/Domain: extracellular #status predicted <TM7-P;210-224/Domain: extr
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F;79-100/Region: hypervariable region HV1
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                                                                                     Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
A;Reference number: S16610; MUID:92114767
A;Accession: S16618
                                                                                                                                                                                                                                                                         C;Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 16-Jul-1999 C;Accession: S16618; A24429; S36328; S28621 R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
                                                                                                                                                                                                                                                                                                                                                                                                                     opacity protein opaC precursor - Neisseria gonorrhoeae
N;Alternate names: opacity protein V0; triosephosphate
C;Species: Neisseria gonorrhoeae
A;Variety: strain_MSll
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A; Molecule type: DNA
A; Residues: 1-260 <BHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LNDKFKPYIGARVAYGHVRHSIDSTKKTTGFLTTAGARGAAPTVSSPYKNTQDAHQESNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 TQSPVKPYLGARLSLN--RASVDF-----126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 DFGGWRIAADYARYRKWNNSKYSVSIKKLQNQYNKKTENQENGTFHAASSLGLSAVYDFK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AEG-ASGFYVQADAAHA------KASSSLGSAKGF-----SPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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28.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (strain MS11) (fragments) dehydrogenase
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A;Cross references: EMBL:X52370
A;Experimental source: strain M511, variant 4.8
A;Note: the authors translated the codon CCA for residue 32 as Thr
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of trans
A;Note: expression of opacity proteins is regulated by the number of trans
A;Note: expression of opacity proteins is regulated by the number of trans
A;Note: the start codon in frame with the rest of the protein R;Stern, A.; Brown, M.; Nickel, P.; Meyer, T.F. Cell 47, 61-71, 1986
A;Title: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic varia A;Reference number: A90887; MUID:87002493
A;Accession: A24429 translated repea

R; Kupsch, uencing

A; Note: this protein is synthesized as a precursor; however, the authors

are uncertai

E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F

A; Molecule type: DNA A; Residues: 25-260 <STE>

DNA

EMBO J. 12, 641-650, 1993

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Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A;Reference number: S16610; MUID:92114767
                                                                                                                                                                          opacity protein opab precursor - Neisseria gonorrhoeae (strain MS11) (fragments) c:Species: Neisseria gonorrhoeae A:Variety: strain MS11 (fragments) A:Variety: strain MS11 (fragments) C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 C:Accession: S16616
                                                                                                                              R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,
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F;102-129/Region: hypervariable region HVI
F;135-149/Domain: transmembrane #status predicted <TM4>
F;155-155/Domain: transmembrane #status predicted <TM5>
F;166-211/Domain: extracellular #status predicted <EXT3:
F;171-217/Region: hypervariable region HV2
F;212-224/Domain: transmembrane #status predicted <TM6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S28617
A; Accession: S28621
A; Molecule type: DNA
A; Residues: 25-260 <MEY>
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A;Accession: S36328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 25-260 <KUP>
Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 ELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 YKVLRTPGAHRESDSIRR--VGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 -----FNGSDSFSQTSTGLGYLAGYSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 SFHAVSSLGLSAIYDFQINDKFKPYIGARVAYGHVRHSIDSTKKITGLLTTSTPGIMSGV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 TDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD------ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 SSILFSSAAQAASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AALIALAHAAALAEGASGFYYQADAAHA------KASSSLGSAKGFS------ 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EASLGVRYRF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.2%; Score 237.5; 29.2%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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F;171-217/Domain: extracellular #status predicted <EXT3> F;176-223/Region: hypervariable region HV2 F;218-230/Domain: transmembrane #status predicted <TM6> F;218-230/Domain: transmembrane #status predicted <TM7> F;234-242/Domain: extracellular #status predicted <TM7> F;243-257/Domain: extracellular #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;258-266/Domain: transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E;101-134/Region: hypervariable region HV1
F;140-154/Domain: transmembrane #status predicted <TM4>
F;160-170/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;95-139/Domain: extracellular #status predicted <EXT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;51-60/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:34-42/Domain: transmembrane #status predicted <TM1>F:43-74/Domain: extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:1-10,11-23/Domain: signal sequence (fragments) #status F:24-266/Product: opacity protein opaD #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain MS11, variant 4.8
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;75-83/Domain: transmembrane #status predicted <TM2>F;88-94/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: opacity protein
C; Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S16616
A; Molecule type: DNA
A; Residues: 1-266 <BHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
246 GRLENTR-FKTHEASLGVRYRF 266
                                                                                                    154 GKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                  111 -----ASVDFNG------SDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYI 153
                                                                                                                                                                                                                                                                                                                                                                                                  126 NIKTRKTEHRENGTFHAASSLGLSAVYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIKELLRNDNANSGGSHL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 -----AKGFSPRISAGYRINDLRFAVDYTRYK-----NYKQVPSTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 KKPSLLFSSALFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTAPKKAQLSTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                             AVTTYPQNAASSVTTNAPIRKLPHHESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNW 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------FKLYSIGASAIYDFDTQSPVKPYLGARLSLNR----- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.2%; Score 237.5; 29.0%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Godayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Cross-references: GB:U32823; GB:L42023; NID:g1574281; PIDN:AAC23104.1; PID:g1574294
                                                                              A; Molecule type: DNA
A; Residues: 1-178 < TIGR>
                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                              A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae A;Reference number: A64000; MUID:95350630
                                                                                                                                                                                                        A; Accession: F64124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: F64124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opacity protein homolog HI1457 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
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Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0
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Match
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105224 seqs, 38719550 residues
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                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation update)
[C precursor (Protein
                                                                                                                              Score 239; DB 1;
Pred. No. 4.1e-14;
                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                               POTENTIAL.
F6B448373830A50D CRC64;
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                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                   Mismatches
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Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q05034;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial cells.";
EMBO J. 12:641-650(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93178439; PubMed-8440254; Rupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; The cell Trapisms displayed by Neisseria gonorrhoeae for human leukocytes and central control of the cell trapisms displayed by Neisseria gonorrhoeae for human leukocytes and central cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae.
Bactaria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Opacity protein OPA67 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane; Multigene family; Signal.
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     127
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                                                                                                                                                                                                                                                                                                              19 AEG-ASGFYVQADAAHA------KASSSLGSAKGF-----SPRISAGY 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
  ----GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                   LNDKFKPYIGARVAYGHVRHSIDSTKKTTGFLTTAGARGAAPTVSSPYKNTQDAHQESNS
                                                                                                                                                    DFGGWRIAADYARYRKWNNSKYSVSIKKLQNQYNKKTENQENGTFHAASSLGLSAVYDFK 121
                                                                                                                                                                                                                                                           SEGNGRGPYVQADLAYAAERITHDYPEATAQKKGTTISTVSDYFRNIRTHSVHPRVSVGY
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                                                                                                                                                                                                                                                                                                                                                                                       27.3%; Score 238.5; 28.3%; Pred. No. 3.
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Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                  32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6C13A46AB163C67F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 233;
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Q57201; O05063;
01-NOV-1997 (Re]
                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJINE-9350630; pubmed-7542800;

**Relaischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
-i- SIMILARITY: WEAK, TO N.GONORRHOEAE OPACITY PROTEINS.
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                      Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20137488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-CCT-2001 (Rel. 40, Last annotation
Protein HI1457 precursor.
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-RD / KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
109 NRASVDENGS----DSF-SQTSTGLGVLAGVSYAVTPNVDLDAGYRXNYIGKVNTVKNVR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION BY MASS SPECTROMETRY.
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                                                                                                                                                                                                                     Local
                                                                                                                                                          1 MKKALAALIALALPAAALAEGASGFYVQA-----DAAHAKASSSLGSAKGFSPRISAG 53
                                                     YAFDKNERLAVDYTNYGKVTANYADVVDVSLKGKSLGLTGFYDFDL-ADFKPYVGVRVST 111
                                                                                    YRIN-DLRFAYDYTRY----KNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSL 108
                                                                                                                       MKKLLIVTMLFTLALSAQAQ-----WYVQGDLGASKIDITHVNSSNS----PSFTQRISVG 52
                                                                                                                                                                                                                                                                                                                                                                             HI1457;
                                                                                                                                                                                                                                                                                                                                                                                          U32823; AAC23104.1; -.
                                                                                                                                                                                                      68;
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                                                                                                                                                                                                                                                                     20 178 F
178 AA; 19470 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10675023;
                                                                                                                                                                                                             27.1%; Score 236.5; 35.4%; Pred. No. 4.2
                                                                                                                                                                                                 24;
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                                                                                                                                                                                                                                                                   15CAC5C44FF49AFF CRC64;
                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                 4.2e-14;
                                                                                                                                                                                                                                DB 1; Length 178;
                                                                                                                                                                                               Indels
                                                                                                                                                                                               31;
                                                                                                                                                                                           Gaps
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                      Best
       Matches
                                  Query Match
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01-OCT-1993 (Rel. 2
01-OCT-1993 (Rel. 2
15-DEC-1998 (Rel. 3
                                                                            VARIANT
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                               Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F., Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
Mol. Microbiol. 6:1073-1076(1992).

-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F., Stern A., Kupsch E.-M., Meyer T.F., Swanson J.; "The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of 11 complete genes."; Mol. Microbiol. 5:1889-1901(1991).
                                                              SEQUENCE
                                                                                                       VARIANT
                                                                                                                      CHAIN
                                                                                                                                               NON_TER
                                                                                                                                                             Outer membrane;
                                                                                                                                                                         InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                     EMBL; Z18939; CAA79372.1; -. EMBL; X60711; CAA43121.1; -. PIR; S28631; S28631.
                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells.";
                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92261323; PubMed=1584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MS11 / V18;
MEDLINE=92114767; PubMed=1815562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Opacity protein OPA60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPAH_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ЕМВО Ј. 12:641-650(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Outer membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGADVTANARYYRIEAFATETRIGIGALAGVQYKLTDNVALNTNIEYNRL-----ASNVS 166
       69;
                   Similarity
                                                                                                                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/
                                                           238 AA;
       Conservative
                                                                                                                    ۵۵
                                                                                                                                                          Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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27,
37,
                 26.8%;
                                                           27073 MW;
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                                                                                   OPACITY PROTEIN (
SED -> MLKA (IN I
V -> M (IN MS11 ,
              Score 234.5; DB 1
Pred. No. 8.8e-14;
                                                                                                                                POTENTIAL
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                                                        883A3560C2DF1B9F CRC64;
    Mismatches
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MS11 / V18).
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81;
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RESULT 6
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DT 01-OCT
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ON OPAJ.
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STRAIN=#831 / F;

STRAIN=#831 / F;

STRAIN=#831 / F;

KUPSCh E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

Evaluation of the state of the state
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Opacity protein OPA58 precursor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; Multigene family; Signal
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PIR; S28624; S28624. 
InterPro; IPR003394; Opacity. 
Pfam; PF02462; Opacity; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIYDFQINDKFKPYIGARVAYGHVRHSIDSTKKTIEVTTVPSNAPNGAVTTYNTDPKTQN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAEGASGFYVQADAAHA------KASSSLGS-----AKGFSPRISAGY 54
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        AVDYTRYKNY---
                                                                                       GPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI 67
                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                          Similarity
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237
237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 26855 MW; B165033B2CBD6A53 CRC64;
                                                                                                                                                                                                                                                                                                      26.8%;
28.6%;
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                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                          Score 234; DB 1;
Pred. No. 9.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
OPACITY PROTEIN OPA58.
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        --- KQVPSTDFKLYSIGASAIYDFDT
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                                                                                                                                                                               -----PRISAGYRINDLRF 61
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01-JUL-1989 (Rel. 11, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                                                                                                                                                              PIR; A24429; KONHO.
PIR; S28621; S28621.
PIR; S36328; S36328.
                                                                                                                                                                                                                                                                             EMBL; M14746; -; NOT_ANNOTATED_CDS. EMBL; Z18927; CAA79360.1; -.
                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stern A., Brown M., Nickel P., Meyer T.F. "Opacity genes in Neisseria gonorrhoeae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOY-1995 (Rel. 32, Last annotation update)
Opacity protein OPA50 precursor (OPA30) (V0) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPAC_NEIGO
                                                                                                  SEQUENCE
                                                                                                                                                 SIGNAL
                                                                                                                                                                                 Outer membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epithelial cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93178439; PubMed=8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87002493; PubMed=3093085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=485;
                                                                                                                                                                 NON_TER
                                                                                                                                                                                                 Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 --GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                              InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 RVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGVRYRF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
   17 ALAEGASGFYVQADAAHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47:61-71(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNTQDAHRESDSIR
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                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                  236 AA;
                                   Conservative
                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                   >236
236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nickel P., Meyer T.F.;
                                                                                                   26685 MW;
                                                  26.5%; Score 231.5; 29.7%; Pred. No. 1.0
                                                                                                                                    OPACITY PROTEIN OPA50
                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
   ---KASSSLGSAKGFS
                                                                                                     68DC237692183398 CRC64;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236
                                                      1.6e-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     control of phase
                                                                     DB 1;
                                      63;
                                                                   Length
                                        Indels
        -PRISAGY
                                      83;
                                      Gaps
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                                                                                                                                            Query Match
Best Local :
                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPAB_NEIGO
Q04874;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MSII / F3;

MEDLINE-93178439; Pubmed-8440254;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

*Variable opacity (Opa) outer membrane proteins account for the c

tropisms displayed by Neisseria gonorrhoeae for human leukocytes

epithelial cells.*;

EMBO J. 12:641-650(1993).

-I- FRNCTEINS. ARE IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA

PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PH
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Opacity protein OPA51 precursor (Fragment)
                                                                                                                                                                                                                                                                                             InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 GSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 AEG-ASGFYVQADAAHA-----KASSSLGSAK------GFSPRISAGYR 55
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FGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTENQENGTFHAVSSLGLSAVY 121
                                                           SEGNGRGPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYD 61
                                                                                                                                                                                                                                                                                                             $28628; $28628.
$36329; $36329.
                                   INDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                           PF02462; Opacity; 1.
membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESDSIRR--VGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIYDFDTQSPVKPYLGARLSLN--RASVD-----FN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENGSFHAVSSLGLS 120
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                                                                                                                                                                                                                                                                                                                                         Z18928; CAA79361.1; -.
                                                                                                                              66;
                                                                                                                                           Similarity
                                                                                                                                                                                      234 AA;
                                                                                                                            Conservative
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                                                                                                                                                                                   26772 MW; 9FFE5B5DABBA96CA CRC64;
                                                                                                                                      26.4%; Score 231; DB 1; 28.2%; Pred. No. 1.7e-13;
                                                                                                                           29;
                                                                                                                                                                                                                 POTENTIAL.
OPACITY PROTEIN OPA51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                         Mismatches
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                              ----KQVPSTDFKLYSIGASAIY 90
                                                                                                                         61;
                                                                                                                                                      Length 234;
                                                                                                                         Indels
                                                                                                                         78;
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EMBO J. 12:641-650(1993).

-i- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MS11 / F3;
MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cropisms displayed by Neisseria gonorrhoeae for human leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27,
01-OCT-1993 (Rel. 27,
01-NOV-1995 (Rel. 32,
                                                           128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z18933; CAA79366.1; -. PIR; S28632; S28632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Opacity protein OPA55
        188
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                                                                                                            128
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                                                                                                                                                               97
                                                                                                                                                                                                  68 AADYARYRKWNDNKYSYDIKELENKNQNKRDLKTENQENGTFHAVSSLGLSAVYDFKLND 127
                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                       24 GFYVQADAAHA-----KASSSLGSAK------GFSPRISAGYRINDLRF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                FOCAT
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                                                                                                                                                                                                                                                                                                   8 GPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI 67
                                             LGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
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LGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Outer membrane.
                                                                                                 KFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEENTQNAHHQSNSIRRVG
                                                                                                                                                          PVKPYLGARLSLN--RASVDF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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234
                                                                                                                                                                                                                                                                                                                                                                                                                                             26.4%;
28.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 230.5; DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPACITY PROTEIN OPA55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 1.9e-13;
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                                                                                                                                                    -NGSDSFSQTST----G 127
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RESULT 11
OP66_NEIGO
ID OP66_NI
AC Q05033
DT 01-OCT
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01-OCT-1993 (Rel. 27, Last ser
01-OV-1995 (Rel. 32, Last ann
Opacity protein OPA56 precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
OP66_NEIGO STANDARD;
Q05033;
01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02462; Opacity; 1.
Outer membrane; Multigene family; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.":
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                  188
                                                                                                                             128 LGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                           128 KFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEENTQNAHHQSNSIRRVG
                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                    PVKPYLGARLSLN--RASVDF------G
                                                                                                                                                                                                                                                                      GPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNVRTHSIHPRVSVGYDFGGWRI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                 AADYARYRKWNDDKYSVDIKELENKNONKRDLKTENOENGTFHAVSSLGLSAVYDFKLND 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S28620; S28620
                                                                                                  LGYIAGYGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGYRYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z18934; CAA79367.1; -.
                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                     234 AA;
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                  >234
234
                                                                                                                                                                                                                                                                                                                                                                                       26868 MW; 5175C6606839EFFB CRC64;
                                                                                                                                                                                                                                                                                                                                            26.4%; Score 230.5; 28.1%; Pred. No. 1.9
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Last annotation update)
precursor (Fragment).
                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.9e-13
                                                                                                                                                                                                                                                                                                                                                                                                                 OPACITY PROTEIN OPA56
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                               PRT;
                                                                                                                                                                                                                                                                                                                                Mismatches
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                                238
                                B
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                                                                                                                                                                                                                                                                                                                                                         Length 234;
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                                                                                                                                                                                                RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA66 precursor (Fragment).
Neisseria gonorrhoeae.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                OPR1_NEIMC P10170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 12:641-650(1993).

-i- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Variable opacity (Opa) outer membrane proteins account for the tropisms displayed by Neisseria gonorrhoeae for human leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelial cells.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Variable opacity (Opa) ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=485;
                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z18941; CAA79374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Outer membrane.
NCBI_TaxID=135720;
[1]
                                                                               Opacity-related protein POPM1.
                                                                                                                                                                                                                                                    188 RRVGLGVIAGVGFDITPNLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 238
                                                                                                                                                                                                                                                                                                                   128
                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GFYYQADAAHA------KASSSLGSAKGF-----SPRISAGYRINDLRF 61
                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                  62 AVDYTRYKNY------KQVPSTDFKLYSIGASAIYDFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GPYVQADLAYAYEHITHDYPKPTDPSKGKLSTVSDYFRNIRTHSIHPRVSVGYDFGGWRI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s28619; s28619. rPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                    ---GLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                   NDKFKPYIGARVAYGHVRHSIDSTKKTTEFLTTAGARGTDPTVSSPYKNTQDAHQESNSI
                                                                                                                                                                                                                                                                                                                                                  QSPVKPYLGARLSLN--RASVDF-----
                                                                                                                                                                                                                                                                                                                                                                                 AADYARYRKWNDSKYSVSIKNIQRRISNGNRRDRKIENQENGSFHAVSSLGLSAVYDFKL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
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238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  >238 OPACITY PROTEIN OPA66.
238
; 26888 MW; B6E38AF1585263AA CRC64;
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27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 229.5;
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                                                                                                                                                                   PRT;
                                  subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                    260
                                                                                                 update)
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Best Local :
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                                  Stern A., Brown M., Nickel P., Meyer T.F.;
"Opacity genes in Neisseria gonorrhoeae: control of phase antigenic variation.";
Cell 47:61-71(1986).
                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                            Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                               NEIGO
                                                                                                                                                                                                         Opacity protein V28 precursor (Fragment).
                                                                                                          MEDLINE=87002493; PubMed=3093085;
                                                                                                                            SEQUENCE FROM N.A.
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Mol. Microbiol. 1:5-12(1987).
-i- SUBCELLULAR LOCATION: Outer membrane.
-i- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPMS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X06445; CAA29748.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                           245 TR-FKTHEASLGMRYRF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                185 GGTPAGGPVIKTDPSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLEN 244
                                                                                                                                                                                                                                                                                                                                                                                                        159 VKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 EHQGNGSFHATSSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Common mechanism controlling phase and antigenic variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88260884; PubMed-2455211;
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        FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KALAALIALALPAAALAEGA-----SGFYVQADAAHA------KASSSLG 41
VARIATION.
                                                                                                                                                                                                                                                                                            NEIGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----YSIGASAIYDFDTQSPVKPYLGARLSLNRA-----SVDFNGS------ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDYFRNIRAHSIHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-----AKGFSPRISAGYRINDLRFAVDYTRYKNYKQVPSTDFKL----------------81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTFSSLLFSSALGAASEDGSRSPYYVQADLAYAAERITHNYPEPTGADKDKISTV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                        PRT;
     PATHOGENESIS AND ARE SUBJECT TO PHASE
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                                                                                                                                                                                                                                                                                        234 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4e-13;
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OP65_NEIGO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                   MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.,
"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
                                                                                                                                                                                                                                                                                                                                                                                           01-OCT 1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA65 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                      Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q04885;
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                                                                                                                        -!- SUBCELLULAR LOCATION: Outer membrane.
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                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 LGYLAGYSYAVTPNYDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
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234
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RESULT 15
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Best Local
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Pfam; PF02462; Opacity; 1.
Outer membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z18940; CAA79373.1; -. PIR; S28617; S28617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q04883;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA59 precursor (Fragment).
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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modulated by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                              Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-MS11 / F3;
MEDLINE=93178439; PubMed-8440254;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                             EMBL; Z18938; CAA79371.1; -. PIR; S28629; S28629.
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             InterPro; IPR003394; Opacity. pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Outer membrane.
Outer membrane;
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| IKPYIGVRVGYGHVRHQVRSVGQETITVTPKPKNGTQGGPVKSTSPIPAVHENRSSRRLG 187
                                                                                                                                                                                                                                                    VARIATION.
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234 AA;
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Multigene family; Signal
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Pred. No. 6.5e-13;
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                                                                                   89 IYDFDTQSPVKPYLGARLSLNR-----
                                                                                                                                                                       8 GPYYQADLAYAYEHITHDYPEPTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI 67
ESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 243
                           DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                             AVDYTRYK-----NYKQVPSTD-------
                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                         1 POTENTIAL.
>243 OPACITY PROTEIN OPA59.
243
a; 27414 MW; 5930C73917436041 CRC64;
                                                                                                                                                                                                                                                25.5%;
                                                                                                                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                Score 223; DB 1; Length 243; Pred. No. 9.2e-13;
                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                     60; Indels
                                                                                         ----- ASVDFNG-----S
                                                                                                                                                 -----FKLYSIGASA 88
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Search completed: October 28, 2002, 16:01:11 Job time: 8.03013 secs

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Result
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Maximum DB
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Copyright (c) 1993 - 2002 Compugen Ltd.
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"Differences in Surface Expression of among NeLsseria meningitidis Group B Infect. Immun. 0:0-0(1999).

EMBL; AF175676, AAD55279.1;

InterProj IPR003394; Opacity.

Pfam; PF02462; Opacity; 1.
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skeiton J., Whitehead S., Spratt B.G., Barrell B.G.;
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                  Martin D., Cadieux N., Hamel J., Rioux C., Bro
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
OUTER MEMBRANE PROTEIN PRECURSOR.
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                                                                                                                                                 STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     STRAIN-Z4063;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; NCBI_TaxID=487, 65699;
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Neisseria meningitidis
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Bacteria; Proteobacteria;
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(TrEMBLrel. 17,
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Best Local :
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Moe G.R., Tan S., Granoff D.M.;
"Differences in Surface Expression of among Neisseria meningitidis Group B Infect. Immun. 0:0-0(199).

EMBL; AF175681; AAD53284.1;
InterPro; IPR003394; Opacity.
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01-MAY-2000
01-MAY-2000
Q9R2R1;
Q9R2R1;
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Bacteria; Proteobacteria;
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EMBL; U52068; AAB41580.1; -.
EMBL; AL162754; CAB84143.1; -.
InterPro; IPR003394; Opacity.
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                                                                                                                                            FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
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174 AA; 1835
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97.18;
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Last annotation updat
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Pred. No. 2.
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Pred. No. 1.
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                         PRT;
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Best Local
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Infect. Immun. 0:0-0(1999).
EMBL; AR175679; AAD53280.1; -
EMBL; AR175677; AAD53280.1; -
InterPro; IPR003394; Opacity.
Pfam; PP02462; Opacity; 1
SEQUENCE 174 AA; 18385 MW; ECF6F3
                                        Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vanathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strair
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed=10710307;
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                      Smith H.O., Frase
"Complete genome
MC58.";
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Bacteria; Proteobacteria; beta sul
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01-MAY-2000
  Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                        G.R., Tan S.,
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96.0%;
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Pred. No. 4.9e-62;
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subdivision;
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"Differences in Surface Expression
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01-JUN-2001
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01-DEC-2001
                                                                                 MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL; AE006143; AAK03109.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPA.
OPA OR PM1025.
Pasteurella multocida.
Bacteria; Proteobacteria;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
01-DEC MEMBRANE PROTEIN PRECURSOR.
   Complete
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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                                      PF02462;
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93.7%;
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EMBL; AF001203; AAC32724.1; -.
InterPro; IPR003394; Opacity.
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U37257; AAC46103.1; -.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Bacteria; Proteobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Z4197;
Hobbs M.M., P
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                           STQNAYHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM
                                            -----DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV
                                                                                 SLGLSAIYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVVTSTHGGADTKPTIYNGE 193
                                                                                                          SIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----
                                                                                                                                                                                           LFSSAAQAASEDSGHGPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH
                                                                                                                                                                                                                      LIALALPAAALAEGASGFYVQADAAHA------KASSSLGS-----AKGFS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGAKVGLRYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNIFDIENKGSNFFRSEKTTKLGYGFIAGAQYGLMTNLFVNGGIEYNRLGRFSDT-SVNQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNRASYDFNGSDSF----SQTSTGLGVLAGVSYAYTPNVDLDAGYRYNYIGKVNTVKNVRS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMRLALDYTHYGKFSGTSYFGVNQKEHVST--KIYGLGLSAFYDFNINSVLKPYVGMRLA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLRFAVDYTRY-----KNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKK----SLLVLAIGALCSLTASANFYVQGDLGVAKTKFSSYSEMNKTNIVPNVSVGYDLG 58
                                                                                                                                     PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS
                                                                                                                                                                PRISAGYRINDLRFAVDYTRYKNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                      256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parachuri P.,
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             Opacity; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α.
                                                                                                                                                                                                                                                                                                      28739 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20512 MW;
                                                                                                                                                                                                                                                             27.7%; Score 242.5; 28.7%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 246; DB 16; 33.5%; Pred. No. 4.6e-13; tive 31; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heckels J.E.,
                                                                                                                                                                                                                                               29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                   OPACITY OUTERMEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                      A5A4F4EFE0E56326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1B17F0A4ACFC0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 AA
                                                                                                                                                                                                                                                             1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Achtman M., cam
k/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                ---KQVPSTDFKLY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cannon
                                                                                                          ----FNGS 118
                                                                                                                                                                                                                                               77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                             Gaps
                                                      171
                                                                                                                                                                                           73
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253 RYHF 256

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RESULT 12
Q9AE80
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Q51124
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DT 01-JU
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DR EMBL;
DR Ffam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
STEAIN-29620;
STEAIN-29620;
MEDLINE-21221108; PubMed-11287631;
Zhu P., van der Ende A., Falush D., Brieske N., Morelli G.,
                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                01-JUN-2001 (TREMBLIEL 17, 01-JUN-2001 (TREMBLIEL 17, 01-DEC-2001 (TREMBLIEL 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q51124;
Q51124;
Q1-NOV-1996
                                                                                                              NCBI_TaxID=487;
                                                                                                                              Bacteria;
                                                                                                                                          Neisseria meningitidis
                                                                                                                                                                      OPACITY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                 Q9AE80;
                                                                                                                                                                                                                                                 Q9AE80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 144:157-166(1998).
EMBL: U37255; AAC46101.1; -.
InterPro; IPRO03394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98129089; PubMed-9467908;
Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
Heckels J.E., Cannon J.G., Achtman M.;
"Recombinational reassortment among opa genes from ET-37 complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis isolates of diverse geographical origins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Z4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                       253 RYRF 256
                                                                                                                                                                                                                                                                                                                                                                          194 PSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM 252
                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 LFSSAAQAASEDSGHGPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LIALALPAAALAEGASGFYVQADAAHA-----KASSSLGS-----AKGFS 47
                                                                                                                                                                                                                                                                                                                                                     RVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                        -----DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                    LGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPTATSPQGGPIIQTD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRVSVGYDFGGWRIAADYASYRKWKESNSSTKKVTEDIADNYKETKTEHQGNGSFHAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRISAGYRINDLRFAVDYTRYKNYKQVPSTDFKL---------YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGASAIYDFDTQSPVKPYLGARLSLNRA----SVDFNGS---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                         Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 AA; 28335 MW;
                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.7%; Score 242.5; DB 2; 27.9%; Pred. No. 1.3e-12;
                                                                                                                          beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                               Created)
                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                             PRT;
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                                                                                                                    subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9D41C6079C6DD13F CRC64;
                                                                                                                                                                                                                                            241 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
                               Bodo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                          epithelial cell invasion.";
Mol. Microbiol. 13:919-928(1994).
EMBL; U13708; AAA74082.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                Pfam; PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                 "The opaH locus of Neisseria gonorrhoeae MS11A is involved
                                                                                                                                                                                                                                                                                                                                                                 Waldbeser L.S., Ajioka R.S., Merz A.J., Puaoi D., Lin L., Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPA15063G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q50943;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S., Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; "Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis."; Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            So M.;
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95115561; PubMed=7815949;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPA15063G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q50943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02462; Opacity; 1.
161 SLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKILTSFYGVATKPTTYDIGP 220
                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ292238; CAC36361.1; -. InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 --DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                              83 SIGASAIYDFDTQSPYKPYLGARLSLN--RASVD-----FNG------ 117
                                                                                      184 YHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGVRYRF
                                                                                                                     41 SLLSAAQAASEAMRGPYVQADLAFAAERITHDYPEPTGTKKGTISTVSDYFRNIRTHSVH 100
                                                                                                                                                   10 ALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAKG------FS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AVYDFNTGSRFKPYAGVRVAYGHVRHSIDSTKKTTNVLTVPTNIPGGTPTIYNQGSTQDA 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 AIYDFDTQSPVKPYLGARLSLN--RASVD----------FN-GS---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 DEGDWRIAADYASYRKWNDNKYSVNTKNVQVNKSNGNRQDLKTENQENGTFHAVSSLGLS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AALAEGA-SGFYVQADAAHA-----KASSSLGS-----AKGFSPRISAGY 54
                                                                                                                                                                                                        ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AASEDGSRSPYYVQADLAYAAERITHDYPKASGANNTSTVSDYFRNIRAHSIHPRVSVGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                         PRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIERVQEAHSNRIDLKAENQENGTFHAVS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RINDLRFAVDYTRYKNY---------KQVPSTDFKLYSIGAS
                                                                                                                                                                                        70;
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AA; 26923 MW; 4923ACF9484BF183 CRC64;
                                                                                                                                                                                                                                                  283 AA;
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.7%;
30.1%;
                                                                                                                                                                                                                                            31877 MW; EBA2AF275316E84B CRC64;
                                                                                                                                                                                                  27.6%; Score 241.5; DB 2; 28.7%; Pred. No. 1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                       26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
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                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 241;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                               Length 283;
                                                                                                                                                                                  79;
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                                                                                                                                                                                Gaps
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           007287
                        O33388;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OPA1700 OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       years of epidemic spread.", Mol. Microbiol. 25:1047-1064 (1997). EMBL; AF001204; AAC32725.1; -. EMBL; AF004823; AAC323684.1; -. InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
Bacteria; Proteobacteria; beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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 Neisseria
             OPAD1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
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                                                                                                                                                                                              124 TSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                           124 DFKLNDKFKPYIGARVAYGYVKHQVQSVESKTKTVTSKPNGGPVKEGPTPKPAYHESNSI
                                                                                                                                                                                                                                                                               64 DFGDWRIAADYASYRKWKESNSSTNTENSETQQNRIKIETGHQGNGSFHAASSLGLSAIY 123
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                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            27.4%; Score 239.5; DB 2; 30.2%; Pred. No. 2.1e-12; on. Mismatches 59;
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the EMBL/GenBank/DDBJ
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Last annotation updat
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SEQUENCE FROM N.A.
STRAIN-FAM 18;
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EMBL; X63108; CAA44822.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitidis.";
Mol. Microbiol. 5:1429-1437(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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259
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                                                STQNAYHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM
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                                                                                                                                                                                PRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                            LFSSAAQAASEDGSRSPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 79
                                                                                                                                                         PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS 139
                                                                           -----DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 171
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262 AA;
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29477 MW;
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5) gene
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y of Neisseria
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Search completed: October 28, 2002, 16:02:38 Job time : 20.0861 secs

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Result
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT: *
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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Neisseria meningit
N. meningitidis 60
MOMP P5. Haemophi
E. Coli cellular p
Salmonella typhi c
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Proteinase K resis
Proteinase K resis
Proteinase K resis
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=	AAY17210	20	704	9.2	79.5	4
	AAG50573	21	645	9.2	•	4
abidopsis tha	AAG50574	21	581	•	•	4
	AAW68202	19	573	٠	79.5	4 2
	AAY97897	21	215	9.3	80.5	4
tinobacillus r	AAY96096	21	215	٠	٠	40
N. meningitidis 60	AAW04909	17	15	9.3	œ	9
igenic	AAU04194	22	282	٠	81.5	
margina	AAB36184	21	282	9.4		3
Anaplasma marginal	AAW51090	19	282	9.4	82.5	36
3	AAG92581	22	261	9.6		ω 5
	AAG32501	21	511	٠	84	34
s thal	AAG09861	21	511	9.7	84	ω ω
11112	AAY97899	21	364	9.7	84	
200	AAY96097	21	364	9.7	84	<u> </u>
Virulence gene pro	AAB44588	21	364	9.7	84	30
Arabidopsis thalia	AAG52874	21	316	9.7	84	29
outer	AAY84612	21	1.80	9.7	84	28
H. pylori bacteria	AAY78360	21	708	9.7		27
Helicobacter pylor	AAW73022	19	708	9.7	84.5	26
Chlamydia trachoma	AAY36955	20	797		æ	25
	AAY34400	20	221	9.9	5	24
nonas din	AAY34533	20	204	•	85.5	23
	AAB65766	22	500	10.0	87	22
Actinobaciling ple	AAY97900	21	369	10.0	87	21
Actinobacillus ple	AAY96098	21	369	•	87	20
Protein associated	AAB59179	22	350	•	87	19
membrane pro	AAP82053	9	350	•	87	18
N. meningitidis 50	AAW04901	17	16	•	87	17
Attachment - three pro	AAR96207	17	162	•	87.5	16
	AAB44589	21	369		89	μ 5
Arabidonsis thalia	AAG09860	21	534	10.3	89.5	14
	28	21	339		S	13
U D D D	AAR66294	16	359	10.5	91	12

ALIGNMENTS

RESULT 1 AAW04893

AAW04893;

AAW04893 standard; Protein; 174

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                                                                                              Brodeur BR, Hamel J, Martin D,
                                        04-AUG-1995;
17-MAR-1995;
                                                                  15-MAR-1996;
                      (IAFB-) IAF BIO VAC INC.
                                                                                                      W05629412-A1
                                                                                                                               Protein
                                                                                                                                                           Key
                                                                                                                                                                                                                 Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                    26-SEP-1996.
                                                                                                                                                Peptide
                                                                                                                                                                         Neisseria meningitidis strain Z4063.
                                                                                                                                                                                                  Proteinase K reistant; Neisseria meningitidis;
                                                                                                                                                                                                                                     22-DEC-1996 (first entry)
                                                                                                                                                                                             Neisseria
                                                                                                                                                                                        gonorrhoeae; antibody; detection; probe; surface protein.
                                       95US-0001983.
95US-0406362.
                                                                  96WO-CA00157.
                                                                                                                               /label= sig_peptide 20..174
                                                                                                                                                        Location/Qualifiers
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    Rioux C;
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strains - useful for prodn. of antibodies for immunisation against,
or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT3903) to AAT39042). The isology to AAT39042 to AAT39042. The isology in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 9; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              may also be used to detect antibodies specific to N. meningitidis
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                                                         04-AUG-1995;
17-MAR-1995;
                                                                                                                                            W09629412-A1
                                                                                                                                                                               Protein
                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                        Neisseria
                                                                                                                                                                                                                                                                           Proteinase K reistant; Neisseria meningitidis;
                                                                                                                                                                                                                                                                                                Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                      AAW04891 standard; Protein;
             Brodeur BR,
                                                                                              15-MAR-1996;
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                                                                                                                                                                                                    Peptide
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                                 (IAFB-) IAF BIO VAC INC
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                                                                                                                                                                                                                                       meningitidis strain 608B.
                                                                                                                                                                                                                                                                gonorrhoeae;
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            Hamel J,
                                                          95US-0001983
95US-0406362
                                                                                              96WO-CA00157
                                                                                                                                                                              /label= sig_peptide
20..174
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                              antibody; detection; probe; surface protein.
             Martin
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Pred. No. 5.8e-85;
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             Rioux C;
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Best Local
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N-PSDB; AAT39039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteinase K reistant;
Neisseria gonorrhoeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteinase K resistant N. meningitidis 22 kD surface protein
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                       Brodeur BR,
                                                                                                                                    04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                                     15-MAR-1996;
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                                                                           (IAFB-) IAF BIO VAC INC
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                       Hamel J,
                                                                                                                                    95US-0001983
95US-0406362
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antibody; detection; pr
                            Martin D,
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Pred. No. 1.8e-83;
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                            Rioux C;
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                                                                                                                                                                                                                                                                                    Proteinase K reistant; Neisseria meningitidi
Neisseria gonorrhoeae; antibody; detection;
                                                                                                                                                                                                                                                                                                                                                      22-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                 AAW04894;
                                                                                                                                                                                                                                                                                                                                                                                                      AAW04894 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7;
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                Brodeur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-443187/44.
                                       (IAFB-) IAF
                                                                  17-MAR-1995;
                                                                              04-AUG-1995;
                                                                                                       15-MAR-1996;
                                                                                                                                 26-SEP-1996
                                                                                                                                                                                               Protein
                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                              Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALATLIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT39040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 8; 117pp; English.
                                                                                                                                                                                                                                                              meningitidis strain b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 AA;
                                        BIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
              Hamel J,
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                95US-0001983.
95US-0406362.
                                                                                                       96WO-CA00157
                                        VAC INC
                                                                                                                                                                                              /label= sig_peptide 20..174
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.6%;
97.1%;
             Martin D,
                                                                                                                                                                                 mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 838.5; DB 1
Pred. No. 8.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                   meningitidis;
              Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                     probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunisation against,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis or
                                                                                                                                                                                                                                                                                     surface protein;
                                                                                                                                                                                                                                                                                                                          protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
AAB19895
ID AAB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection
                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Fig 10; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-443187/44.
N-PSDB; AAT39042.
                                                                                                                                                                                                                                                                        Neisseria
                                                                                                                                                                                                                                                                                                NspA; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis NspA
                                                                                                                                                                                                                                                                                                                                                                              AAB19895;
                                                                                                                                                                                                                                                                                                                                                                                                      AAB19895 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences encoding the antigen, or their fragments, can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may also be used to detect antibodies specific to N. meningitidis
Region
                         Region
                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ш
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt MKKALAALIALAPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                        meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the detection
                      /note= "s
                                                                                                     /note=
63..74
                                                   /note=
89..10
                                                                          /note=
78..88
                                                                                                                                                                               /note=
27..37
                                                                                                                                                                                                       /note=
18..26
                                                                                                                                                    40..50
                                                                                                                                         /note=
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.1%;
95.4%;
                                    "surface-exposed connecting
                                                              "transmembrane beta-strand"
                                                                                                                                                                                                                   "transmembrane beta-strand"
            "transmembrane beta-strand"
                                                                                                                                                                 "transmembrane beta-strand"
                                                                                                                                                                                          "surface-exposed connecting
                                                                                       "transmembrane
                                                                                                               "surface-exposed connecting
                                                                                                                                         "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                therapy; vaccine; meningococcal B.
                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 834; DB Pred. No. 2.6e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of pathogenic Neisseria bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                       beta-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17;
.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                 loop'
                                                                                                                                                                                           loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The antigen
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Gaps

0

60

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POPM3

vaccine; AS; RV-1;

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RESULT 6
AAR73911
ID AAR7
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         D X A X
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                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            (iii) mixtures of 1 or more Neisserial protein and 1 or more Neisserial protein and 1 or more Neisserial space and 1 or more Neisserial space and nucleic acids are preferably from different Neisseria spp., especially Neisseria meningitidis and Neisseria gonorrhoeae, but may be from the same species. A claimed composition includes the NspA protein, preferably in mature form. The compositions are used e.g. as immunogenic compositions, vaccines or diagnostic reagents. They are used to treat or prevent Neisserial infection, to detect the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria, and/or as reagents which can raise antibodies
         05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                AAR73911 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, which contains 8 transmembrane beta-strands and 4 surface-exposed connected loops. Recombinant NspA is being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of the Neisseria meningitidis NspA protein, which contains 8 transmembrane beta-strands and 4 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition comprising first and second biological molecules from a Neisseria bacterium, useful as vaccines or immunogenic compositions for treating Neisserial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   against Neisserial bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                combination compositions comprising: (1) 2 or more Neisserial proteins, (11) 2 or more different Neisserial nucleic acids, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease caused by all serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-2000; 2000WO-IB00828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200071725-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developed as a vaccine for the prevention of meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Fig 32; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1999;
19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
                                                                                                                                             121
                                                                                                                                                          140 NVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                       61
                                                                                                                                                                                                                                     08
                                                                                                                                                                                                                                                                                20 EGASGFTYQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 79
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                      LYSIGASAIYDEDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTP 139
                                                                                                                                                                                                                                                                EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFK
                                                                                                                                                                                                      LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-025167/03
                                                                                                                                            NVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 155
                                                                                                                                                                                                                                                                                                                              152;
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                        155 AA;
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000GB-0005730
      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99GB-0011692.
99GB-0019705.
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146..1
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131..145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 155
                                                                                                                                                                                                                                                                                                                                          88.8%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "surface-exposed connecting
                                                                  170
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                          Score 771;
Pred. No. 1
                                                                  A
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides
                                                                                                                                                                                                                                                                                                                                          DB 22;
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••
                                                                                                                                                                                                                                                                                                                                                       Length 155;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     loop"
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                  AAW04912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR73911 is the Neisseria meningitidis opacity related protein POPM3. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73889 and AAR73901, which are recognised by a monoclona antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis treatments. The peptides may also be used as vaccines against meningitis.
                 Proteinase K reistant;
                                               N. meningitidis 608B peptide CS-857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis - the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharma LR, Van Alstyne
                                                                              22-DEC-1996
                                                                                                                                        AAW04912 standard; Protein; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 47; Fig 5/10; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) and corresp. antibodies for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHAR/) SHARMA L R. (VALS/) VAN ALSTYNE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; opacity related protein POPM3; meningitis related homologous antigenic sequence; MRHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis opacity related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoassay;
                                                                                                                                                                                                                    135
                                                                                                                                                                                                                                                08
                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                   6 ATLIALALPAAALAEGASGFYVQADAAH-----AKASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                  ASSLGLSATYDFKLKGKFKPYIGARVAYGHVRHSID
                                                                                                                                                                                                                                               LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                         FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                       SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                                                                                                           IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                    41;
    gonorrhoeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and preventing meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; treatment; prophylactic; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0127499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-CA00516.
                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%;
Neisseria meningitidis; epitope; mapping; antibody; detection; probe; surface prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ď,
                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                              Score 135; DB 10;
Pred. No. 1.8e-06;
Pred. No. 1.8e-47;
                                                                                                                                                                                                                  170
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Length 170; Indels

monoclonal

for

48;

Gaps

4:

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RESULT 8
AAB47447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             surface exposed loop; major outer membrane protein P5; MOMP P5;
non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
otitis media; sinusitis; conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB47447 standard;
        23-AUG-2001.
                               WO200161013-A1
                                                                                   Domain
                                                                                                                        Domain
                                                                                                                                                                 Domain
                                                                                                                                                                                                                  кеу
                                                                                                                                                                                                                                             Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9 describes the epitope mapping of the 22 kD N. meningitidis protein. Identification was accomplished using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection
                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                       Lower
                                                                                                                                                                                                                                                                                                                                        MOMP
                                                                                                                                                                                                                                                                                                                                                                                          AAB47447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Page 84; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IAFB-) IAF BIO VAC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FAVDYTRYKNYKAPSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                      respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0001983.
95US-0406362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-CA00157
                                                                                            /note= "Extracellular
                                                                                                         /label=_Loop 3
                                                                                                                                  /note= "Extracellular domain"
                                                                                                                                                                          note= "Extracellular domain"
                                                                                                                                                                                       /label= Loop 1
                                                                                                                                                                                                                 Location/Qualifiers
                                                      'note= "Extracellular domain"
                                                                      'label=
                                                                                                                                                   /label- Loop 2
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                               00
                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 133; DB 17; 100.0%; Pred. No. 2.3e-07;
                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin
                                                                    Loop 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                   353 AA
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                                                                                              domain*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                               AAU34556
ID AAU3
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the major outer membrane protein P5 of non-typeable H. influenzae. One or more surface exposed loops of this protein may be replaced with a modified peptide of the invention. Each of these peptides contain an LB1[f] peptide which is a 19 amino acid peptide derived from the sequence of MOMP P5 from strain ntHill28, representing amino acids Arg117 to G1y135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP P5 may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., ocitis media, sinusitis, conjunctivitis, or lower
                                                                         Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
27-SEP-2001
                                                                                                               E. coli cellular proliferation protein #137.
                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                 Escherichia coli
                                                                                                                                                                      AAU34556;
                                                                                                                                                                                            AAU34556 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     otitis media and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berthet FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2001; 2001WO-EP01556
                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                            181 LTRYGKYRPODKPNTALNYNPWIGSINAGISYRF 214
                                                                                                                                                                                                                                                                                                             121 DVYGKAGVALVRSDYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLEYQW 180
                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                               61 YGVFGGYQILNQNNLGLAVELGYDDFGRAKGREKGKTVVKHTNHGTHLSLKGSYEVLEGL 120
                                                                                                                                                                                                                                                                                                                                                                                          48 PRISAGYRI---NDLRFAV-----DYTRYKNYKAPSTDFKLYSIGA--SAIYDFDTQSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKALATLIALALPAAALAEGA---SGFYVQADAAHAKASSSLGS-----AKGFS
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQASFHDGLRALAREYKVGYHRNSFT
                                                                                                                                                                                                                                                                                                                                      KPYLGARLSLNRASVDLGGSDSFSQTSTG-----LGVLA-GVSYAVTPNVDLDAGY--
                                                                                                                                                                                                                                                                                     ----RYNYIGKVNTVKNVRS--GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-0003502
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                                                                                                                                                                                              212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99;
Pred. No.
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                                                                                      protein;
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Gaps

9;

97 60

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AAU38252
ID AAU3
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AC AAU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes themselves and the discovery of novel antibiotics, the essential coc genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella coc invention is also useful for the identification of potential new targets coc invention is also useful for the identification of potential new targets coc inventify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery compositions nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an cessential prokaryotic cellular proliferation protein.

Conte: The sequence data for this pattent did not form part compounds in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-2000;
22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Seq ID No 10149; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibiotics, comprise sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIT-)
               AAU38252;
                                              AAU38252 standard; Protein; 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                             169 WLVNMSVWYMDIDTTANYK-LGGAQQHDSVRLDPWVFMFSAGYR 211
                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                     1 MKKALATLIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                       1 MKKLTVAALAVTTLLSGSAFAHEAGEFFMRAGSATVRPTEGAGGTLGSLGGFSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-611495/70.
                                                                                                                                                                                           YFGDASSKFRPYVGAGINYTTFFDNGFNDHGKEAGLSDLSLKDSWGAAGQVGVDYLINRD
                                                                                                                                                                                                                         ---DTQSPVKPYLGARLS-----LNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPN 140
                                                                                                                                                                                                                                                                                       RINDLRFAVDYTRYKNYKA------PSTDFKLYSIGASAIYDF------
                                                                                                                                                          -----VDLDAGYRYNYIGKVNTVKNVRSGE----LSAGVR 171
                                                                                                                                                                                                                                                         -TNNTQLGLTFT----YMATDNIGVELLAATPFR-HKIGTRATGDIATVHHLPPTLMAQW
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                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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2000US-207727P.

2000US-242578P.

2000US-253625P.

2000US-257931P.

2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 AA
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                                                                                                                                                                                                                                                                                                                                                                                                    11.1%;
23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     77; Indels
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                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, themselves and the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                    Query Match
Best Local
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhi cellular proliferation protein #143.
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                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Seq ID No 13845; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
135 YFGDSSSKYRPYVGVGVNYTTFFDNDFNDNGKKTGLSDLSFKDSXGAAGQVGVDYLINRD
                                 92
                                                                  82
                                                                                                    55
                                                                                                                                   27
                                                                                                                                                                   1 MKKALATLIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-611495/70.
                                                                                                                                   MKKFTVAALALTTLLSGSAFAHEAGEFFMRAGPATVRPTEGAGGTLGHLNGFD--VS---
                               ---DTQSPVKPYLGARLS-----LNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPN 140
                                                                                                  RINDLRFAVDYTRYKNYKA------PSTDFKLYSIGASAIYDF------
                                                                 --NNTQLGLTFT----YMATDNIGVELLAATPFR-HKVGTGATGDIATVHLLPPTLMAQW 134
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prokaryotic cellular proliferation protein
                                                                                                                                                                                                                                                                       257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                                                                                                     Conservative
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Xu HH;
                                                                                                                                                                                                                    10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind
                                                                                                                                                                                                      28; Mismatches
                                                                                                                                                                                                                    Scorè 92; DB 2
Pred. No. 0.13;
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RESULT 11
AAR96210
ID AAR96
      The sequence represents a fusion protein of a versinia centerocolitica attachment-invasion-locus (AIL) protein (AAR96207) With maltose binding protein (MBP, AAR96208). The MBP N-terminal portion of the fusion protein acts as an affinity tail, allowing chromatography. The receptor binding region of the AIL protein combinant protein purification by amylose affinity chromatography. The receptor binding region of the AIL protein involves all or some of the regions from the 4 extracellular loops. This region retains the binding affinity of the protein, and may be used alone or as part of a fusion protein for drug delivery. The transport the agent across the gastrointestinal membrane barrier by transports to increase bioavailability 5- to 100-fold. The delivery system allows improved transport across enterocytes and eyers patch M-cells. The system is not prone to degradation in the
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                                                                                                                                                                                                                                                                                     Therapeutic delivery system utilising bacterial invasin protein - in not readily degraded in the gut, enhances systemic bio-availability
                                                                                                                                                                                                                                             Example 3; Fig 15; 110pp; English.
                                                                                                                                                                                                                                                                             of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                        Habberfield AD,
                                                                                                                                                                                                                                                                                                                                           WPI; 1996-251447/25.
                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9613250-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attachment-invasion-locus protein; maltose binding protein; fusion protein; affinity tail; amylose; affinity chromatography; purification; drug delivery; gastrointestinal membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIL protein-maltose binding protein fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR96210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR96210 standard; Protein; 568 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 WLIGASVWYMDIDTTANYK-MGGVQQHDSVRLDPWVFMFSAGXR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 -----VDLDAGYRYNYIGKVNTVKNVRSGE----LSAGVR 171
 early release of biologically active material,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug delivery; gastrointestir
bioavailability; enterocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0331393
                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US13749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508..525
                                                                                                                                                                                                                                                                                                                                                                   Jensen-Pippo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464..482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . . 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Maltose binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Attachment-invasion-locus protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Peptide from extracellular loop-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Peptide from extracellular loop-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Peptide from extracellular loop-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from extracellular loop-3"
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
The fimbrin proteins from 15 randomly selected type b and non-typable clinical isolates of Haemophilus influenzae share common epitopes. Thus frimbrin isolated from non-typable Haemophilus influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause otitis media. Fimbrin protein is produced by culturing a transformed microbial host , pref. E.coli, Sporodoptera frugiperda or a mucosal
                                                                                                                                        Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
                                                                                                                 Disclosure; Fig 5; 45pp; English.
                                                                                                                                                                                                      N-PSDB; AAQ78916
                                                                                                                                                                                                                  WPI; 1995-006359/01.
                                                                                                                                                                                                                                            Bakaletz LO,
                                                                                                                                                                                                                                                                                                    18-MAY-1993;
                                                                                                                                                                                                                                                                                                                               12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                           24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                     W09426304-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fimbrin protein; vaccine; otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-typable Haemophilus influenza (NTHi) fimbrin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR66294;
                                                                                                                                                                                                                                                                        OHIO-) OHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR66294 standard; Protein; 359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eliminates the need for parenteral administration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 LGAGYR 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ALPAAALAEGASGFYYQADAAHAKASSSLGSA------KGFSPRISAGYRI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKVKASV---FDESISASKTSMAYGAGVQFNPLPNFVIDASYEYS---KLDSIK-VGTWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDNWGVIGSFA--YTHQGYDFFYGSNKFGHGDVDYYSVTMGPSFRINEYVSLYGLLGAAH 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPGRGSIEGRASVNVY---AASESSISIGYAQSHVKENGYTLDNDPKGFN--LKYRYEL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDL-----RFAVDYTR-----YKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenza strain 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                       STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                            Kolattukudy PE,
                                                                                                                                                                                                                                                                                                 93US-0065442.
                                                                                                                                                                                                                                                                                                                               94WO-US05477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            /label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= amino terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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Pred. No. 0.37;
                                                                                                                                                                                                                                           Sirakova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                           Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 13
AAG52873
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អនុស្វ
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     Query Match
Best Local S
Matches 54
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

23-MAR-1999

24-MAR-1999

01-APR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

25-APR-1999

26-APR-1999

27-APR-1999

28-APR-1999

29-APR-1999

30-APR-1999

30-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogen. Fimbrin protein (FP) produced by this process is claimed. The FP protein migrates in polyacrylamide genes to a posn. equiv. to a mol. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rsucein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 67258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG52873 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 YAVLPELAVRLEYQWLTRYGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALATLIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARLSLNRASVDLGGSDSFSQTSTGL--------GVLA-GVS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAVTPNVDLDAGY -----RYNYIGKVNTVKNVRS--GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AYLSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRRNTFTYGV----FGGYQILNQD----NFGLAAELGYHDFGRAKLREAGKPKAKHTNHG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
 99US-0121825.
99US-012548.
99US-0125788.
99US-0126764.
99US-0127762.
99US-0127762.
99US-0127762.
99US-0128734.
99US-0130077.
99US-013049.
99US-013049.
99US-013048.
99US-013248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
   3-0130510

3-0130891

3-0131449

3-0132048

3-0132487

3-0132484

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5-0125788.

5-0126264.

5-0126785.

5-0127462.

5-0128234.

5-0128714.

5-0128714.

5-0128717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91; DB 16; Length 359; Pred. No. 0.26;
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       20-MAY-1999

21-MAY-1999

24-MAY-1999

25-MAY-1999

27-MAY-1999

01-JUN-1999

01-JUN-1999

01-JUN-1999

01-JUN-1999

10-JUN-1999

10-JUN-1999

10-JUN-1999

11-JUN-1999

11-JU
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14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
       19-JUL-1999
19-JUL-1999
19-JUL-1999
20-JUL-1999
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99US-0134214.
99US-0134276.
99US-0134276.
99US-0134276.
99US-013523.
99US-013523.
99US-013622.
99US-013622.
99US-013622.
99US-0137528.
99US-0139452.
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99US-0139457.
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99US-0139461.
99US-0139461.
99US-0139461.
99US-0139461.
99US-0140833.
99US-0140833.
99US-0140834.
99US-0144334.
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                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                       termination sequence.
                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 7956.
                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            AAG09860;
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1 Similarity 27.7%; Pred. No. 0.35;
39; Conservative 20; Mismatches 53;
9908-0121825

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from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and
                                                              The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes
                                                                                                       Claim 39; Pages 308-309; 322pp; English.
                                                                                                                                          Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                              Lowery DE,
                                                                                                                                                                                                                                                                                                                                                                                                                        Virulence gene; antibacterial; vaccine; septicemia; bronchopneumonia; rhinitis;
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                              Actinobacillus pleuropneumoniae
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                                                                                                                                                                                                                            Kennedy MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial infection;
wound infection.
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177 ELAARVEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRF 224
                               142 DLDAGYRYNYIGKVNTVKN--VRSG------ELSAGVRVKF 174
                                                               119 PSYEVLPDLDVYGKVGIAVVRNDYKKYGAENTNESTTKFHKLKASTILGAGVEYAILP--
                                                                                               90 -DFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGVL-----AGVSYAVTPNV 141
                                                                                                                              59 YGINRNSVTYGVFGGYQILNQNNFGLAAELGYDYYGRVRGNVDEFRTVKHSAHGLNLALK 118
                                                                                                                                                              50 -----ISAGYRI----NDLRFAVD--YTRYKNYKAPSTDFKLYSIGASAIY---- 89
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                              1 MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                                                                                                                                                                                                                               1 MKKALATLIALALPAAALAEGA~--SGFYVQADAAHAKASSSLGSAK-GFSPR----- 49
                                                                                                                                                                                                                                                                                                                                            369 AA;
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Search completed: October 28, 2002, 16:00:39 Job time: 25.7145 secs

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Result
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Perfect score:
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1: /cgn2_6/ptodata/:

2: /cgn2_6/ptodata/:
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US-09-336-447A-1
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ALIGNMENTS

US-08-913-362-6

Sequence 6, Application US/08913362 Patent No. 6287574
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernar APPLICANT: Martin, Denis APPLICANT: Hamel, Josee APPLICANT: Rioux, Clement

Brodeur, Bernard R

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

ADDRESSEE:

E: Foley & Lardner 3000 K Street, N.W., Suite 500

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; MOLECULE TYPE: US-08-913-362-6
     Query Match
                                                                                                                                  TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 PRIOR APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-WAR-1995 PRIOR APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-WAR-1995 PRIOR APPLICATION NUMBER: US 60/001,983
                                                                                                                                                     TELEPHONE: (202)672-5399
TELEX: 904146
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                   FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polo-
                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
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                                                                                               174 amino acids
                                                                      linear
                                                 protein
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Patent No. 6287574
                                                              Matches
                                                                                      Query Match
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
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                                                                         Local Similarity
                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                              TELEFAX:
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              1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                              : (202)672-5300
(202)672-5399
                                                              Conservative
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                                                                            Score 854; DB 4;
Pred. No. 2.3e-90;
                                                              Mismatches
                                                                                         Length 174;
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                                                                                                                                                                                               Matches 172;
                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 0479
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
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TELEFAX: 904136
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                  120 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/C
FILING DATE: 13-NOV-1997
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                                                   61 FAVDYTRYKNYKXAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                  61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                        1 MKKALATLIALALPAAALAEGASGFYVOADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                      1 MKKALAXLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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o. 6287574
20007-5109
                                                                                                                                                                                                                                                                                                                                    amino acid
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                    175 amino acids
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                                                                                                                                                                                                                                                                                   protein
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Sequence 8, Application US/08913362 Patent No. 6287574
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0479
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
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PRIOR APPLICATION UMBER: US 08/406,362
                                                                                FILING DATE: 17-MAR-PRIOR APPLICATION DATA:
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APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                              61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
                                                                                                                                                               61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
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                                                                                                                                                                                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                  Local Similarity
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3000 K Street, N.W., Suite 500
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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RESULT 6
US-08-127-499A-20
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                                                                                                            Sequence 20, Application US/08127499A Patent No. 5510264 GENERAL INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
             APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH
TITLE OF INVENTION: HOMOLOGOUS ANTIGE
NUMBER OF SEQUENCES: 40
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
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APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
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COMPUTER READABLE FORM:
MENTIM TYPE: Floppy disk
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APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
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APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                  121 SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                          121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                           61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 174 amino TYPE: amino acid
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OPERATING SYSTEM:
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Local Similarity 95.4%;
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3000 K Street, N.W., Suite 500
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SYSTEM: PC-DOS/MS-DOS
                               ANTIBODIES WHICH BIND MENINGITIS RELATED HOMOLOGOUS ANTIGENIC SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acid
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESEI
TITLE OF INVENTION: BACTERIAL AND VII
TITLE OF INVENTION: CNS CARRIER, ANT
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MEDIUM TYPE: Floppy disk
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                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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STREET: 30
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                          STREET:
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APPLICATION NUMBER: US/C
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 amino acids
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(202)672-5399
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                                                                                                                                                                                                                                                           Foley & Lardner
                                                                                                                                                                                                                                                                                                                                          PEPTIDES RÉPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
                                                                                                                                                                                                                                                                                                                       CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 135; DB 1; Length 170; 26.3%; Pred. No. 8.2e-08;
                    US/08/482,847
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A.
REGISTON NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
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APPLICANT:
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                                                                                                             APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEINASE K RESISTANT SU
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                             PRIOR APPLICATION DATA:
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TELEX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                           APPLICATION NUMBER:
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Rioux, Clement
RYENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202)672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brodeur,
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                                                                                                                                                                                                                                                                                          Floppy disk
                                                        UMBER: US 60/001,983
04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%; Score 135; DB 1; 26.3%; Pred. No. 8.2e-08;
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; ORIGINAL SOURCE:
; ORGANISM: Neisseria m
; STRAIN: 608B
US-08-913-362-26
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                                                                                                                   Matches
                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                   TELEFAX: (216) 241-0816
INFORMATION FOR SEO ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLTICK, MATY E.
REGISTRATION NUMBER: 34,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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54 YRINDLREAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL----G 102
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                                 1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                     1 MKKALATLIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 15.3%; Score 133; DB 4; Local Similarity 100.0%; Pred. No. 7.8e-09; Local Similarity 0, Mismatches 0;
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                                                                                                                 Conservative
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                                                                                                                             10.7%; Score 93; DB 1; Length 359; 23.6%; Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/457,997B
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                                                                                                        28; Mismatches
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                                                                                                      83; Indels 64; Gaps
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US-08-467-722A-2
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TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: GOLTACK, MATY E. REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEPHONE: (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
172 YAVLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                    135 YAVTPNVDLDAGY-----RYNYIGKVNTVKNVRS--GELSAGVRVKF 174
                                                                         112 AYLSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAE 171
                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 YAVLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                                                                                                                                   60 YRRNTFTYGV----FGGYQILNQD----NFGLAAELGYDDFGRAKLREAGKPKAKHTNHG 111
                                                                                                                                                                                       54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL-----G 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 YAVTPNVDLDAGY-----RYNYIGKVNTVKNVRS--GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AYLSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                            1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
                                                                                                                                                                                                                                                                 1 MKKALATLIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Suite 1
CITY: Cleveland
                                                                                                                                                                                                                                                                                                                            Match 10.7%; Score 93; DB 3; Length 359; Local Similarity 23.6%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                83;
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RESULT 11

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PCT-US95-13749-5
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US-08-913-362-15
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GENERAL INFORMATION:
APPLICANT: Amgen Inc.
APPLICANT: Amgen Inc.
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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APPLICANT: Brodeu
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                           APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              562 LGAGYR 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 LSAGVR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 SLNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 DDNWGVIGSFA--YTHQGYDFFYGSNKFGHGDVDYYSVTMGPSFRINEYVSLYGLLGAAH 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 SVPGRGSIEGRASVNVY---AASESSISIGYAQSHVKENGYTLDNDPKGFN--LKYRYEL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 NDL----RFAVDYTR-----YKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ALPAAALAEGASGFYVQADAAHAKASSSLGSA------KGFSPRISAGYRI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 10.6%; Score 92; DB 5; Local Similarity 25.8%; Pred. No. 0.043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                        STREET: 3000 K STREET: Washington
                                     COUNTRY:
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                                         USA
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RESULT 13
US-08-733-230-6
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US-08-913-362-15
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Patent No. 602533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
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LENGTH: 16 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-NOV-1997 PRIOR APPLICATION DATA:
                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,230
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                             STREET: 2421
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                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                     FILING DATE:
                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                 ADDRESSEE:
                CLASSIFICATION: 514
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                                                                                                                                                                              32606
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2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                                                         McGuire, Travis C.
Burridge, Michael J.
                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ganta, Roman Reddy
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CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 282
TYPE: PRT
                                                                                                                           Matches
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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LENGTH: 282 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 PVSPYVCA--GIGASFVDIS-----KQVTTKLAYRGKVGISYQFTPEISLVAGGFYHGLF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 --RFATLADGQYAKSGAESLAAITRDANITETNYFVVKIDEITNTSVMLNGCYDVLHTDL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
         58 DLRFA---
                                 80 KSIAT-IDVSVPANFSKSGYTFAFSKNLITSFDGA---VGYSLGGAR---VELEASYR-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 DESYKDIPAHNSVK--FSGEAKASVK 265
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 PVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGV--LAGVSYAVTPNVDLDAG------ 146
                                                                     3 KALATLIALALPAAALAEG-----ASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRIN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 DLRFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 KSIAT-IDVSVPANFSKSGYTFAFSKNLITSFDGA---VGYSLGGAR---VELEASYR-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KALATLIALALPAAALAEG-----ASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRIN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Whitlock, Ted W. 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352-372-5800
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                                                                                                                               9.4%; Score 81.5; DB 4; Length 282; 25.2%; Pred. No. 0.24;
-----VDYTRYKNYKAPSTDFKLYSIGASAIYD-FDTQS 95
                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VDYTRYKNYKAPSTDFKLYSIGASAIYD-FDTQS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.5; DB 3; Length 282; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UF-167
                                                                                                                 Mismatches
                                                                                                           75; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                           Gaps
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US-08-913-362-23
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                                                                  Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6287574
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23,
                                                                                                                                                                                                                                                     TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                              MOLECULE TYPE: FORIGINAL SOURCE: ORGANISM: Neis STRAIN: 608B
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                             141 VDLDAGYRYNYIGKV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 PVSPYVCA--GIGASFVDIS-----KQVTTKLAYRGKVGISYQFTPEISLVAGGFYHGLF 241
1 VDLDAGYRYNYIGKV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 DESYKDIPAHNSVK--FSGEAKASVK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 -YRYNYIGKVNTVKNVRSGELSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 --RFATLADGQYAKSGAESLAAITRDANTTETNYFVVKIDEITNTSVMLNGCYDVLHTDL 188
                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                              Local Similarity
                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 PVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGV--LAGVSYAVTPNVDLDAG----- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                             15; Conservative
                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08913362
                                                                                                                                                                                                                                              15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamel, Josee
Rioux, Clement
                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                                               Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brodeur, Bernard R
                                                                                                                                                                                             protein
                                                      100.08; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                              us 60/001,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/913,362
                                                                                                                                                                                                                                                                                                                                                                        29,768
                                                                       Score 81; DB 4; Length 15; Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                          047998/0128
                                                             Mismatches
                                                       0;
                                                      Gaps
                                                       0,
```

Search completed: October 28, 2002, 16:04:20 Job time : 10.4864 secs

```
OM protein - protein search, using sw model
                                                          October 28, 2002,
                                                                                                                                                                                   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
15:58:04 ; Search time 12.4821 Seconds (without alignments)
1339.485 Million cell updates/sec
```

Perfect score: US-09-684-883-6 868

MKKALATLIALALPAAALAE.....VNTVKNVRSGELSAGVRVKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* pir1:*
pir2:*
pir3:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query	æ		
		SUMMARIES	
		RIES	

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	<u>.</u>	12	11	10		. 00	7	ı o	, UT	4	·w	N	1	No.	
214	219	220	222	223.5	225	225	225	225	230	231	231	231.5	231.5	235	235.5	236	236	237	238	239.5	239.5	240	240	240.5	241	243.5	858	868	Score	
24.7	25.2	25.3	٠	•	•	٠	•	•	•	٠	26.6	٠	•	•	27.1	27.2	•	27.3	•	•		•	27.6	•	•		•	100.0	Query Match I	de .
	238										234																		Length DB	
				2 S36346							2 \$36342				1 KONH2C	2 \$04380						1 KONHO	2 S16612			2 \$16610			di.	5
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protein	protein	protein	protein		protein	protein	protein	protein	protein	protein		protein	protein	protein	protein	protein	protein	protein-	protein		protein	protein		protein	protein	ty protein	membrane	outer membrane pro	on	

45	44	3	42	41	40	39	ω 8	37	36	ω	34	w	32	ω	30
122.5	122.5	124	126	126.5	130.5	130.5	132	135	135	138	151.5	177.5	190.5	205.5	207.5
14.1	14.1	14.3	14.5	14.6	15.0	15.0	15.2	15.6	15.6	15.9	17.5	20.4	21.9	23.7	23.9
264	70	284	192	201	284	281	239	170	168	187	210	121	235	247	214
Ν	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
I54668	F64066	AG3556	S44712	S16286	G98271	AH3012	AH0541	T10256	S08513	S20044	S77737	164187	S44707	S28627	S44706
heat resistant agg	probable outer mem	heat resistant agg	opacity protein op	opacity protein op	hypothetical prote	outer surface prot	probable outer mem	opacity protein-re	opacity protein-re	opacity protein op	opacity protein op	opacity protein ho	opacity protein on	opacity protein op	opacity protein op

ALIGNMENTS

RESULT 1

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain 72491 sero C;Dspecies: Neisseria meningitidis C:Dspecies: Neisseria meningitidis C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: B81932

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491 A;Reference number: A81775; MUID:20222556 A;Accession: B81932 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <PAR>

A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84143.1; PID:g737 A;Experimental source: serogroup A, strain Z2491

A; Gene: nspA; NMA0862 C; Genetics:

밁 밁 Ω В Š Matches Query Match 121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174 121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60 Local Similarity 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60 174; Conservative 100.0%; Score 868; DB 2; 100.0%; Pred. No. 2.9e-69; tive 0; Mismatches 0; Length 174; Indels 0; Gaps 0;

outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58 C.Species: Neisseria meningitidis
C.Species: Neisseria meningitidis
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C.Accession: G81174
R.Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Saliberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
A;Accession: G81174

A;Status: preliminary

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RESULT 3
S16610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;76-84/Domain: transmembrane #Status predicted <TM2>
F;89-95/Domain: transmembrane #Status predicted <TM3>
F;89-95/Domain: extracellular #Status predicted <EXTZ>
F;96-134/Domain: extracellular #Status predicted <EXTZ>
F;102-129/Region: hypervariable region HVI
F;135-149/Domain: transmembrane #Status predicted <TM4>
F;155-165/Domain: transmembrane #Status predicted <TM5>
F;155-165/Domain: transmembrane #Status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C: Keywords: cell surface component; transmembrane protein F;1-10,11-23/Domain: signal sequence (fragments) #status F;24-261/Product: opacity protein opak #status predicted <F;34-42/Domain: transmembrane #status predicted <FM1>F;34-42/Domain: extracellular #status predicted <FM1>F;43-75/Domain: extracellular #status predicted <FM1>F;51-61/Region: semivariable region F;51-61/Region: semiv
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A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-174 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: strain MS11, variant 4.8
A;Note: the authors did not translate the sequence for the signal peptide A;Note: expression of opacity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam
A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;116-212/Domain: extracellular #status predicted <EXT3>
F;171-218/Region: hypervariable region HV2
F;213-225/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: opaK
C; Superfamil
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A; Residues: 1-261 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 13-Jan-1995
C; Accession: S16610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opacity protein opaK precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N;Alternate names: outer membrane protein opaK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          닭
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;229-237/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X52364
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     밁
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Best Local
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                                                                                                                                                                                                             Matches
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          21
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                                                                                                            15 AAALAEG-ASGFYVQADAAHAKA-----SSSLGSAKG------
                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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{\tt AQAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKGTTISTVSDYFRNIRTHSIHPRV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172;
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98.9%;
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                                                                                                                                                                                                                                                              Score 243.5;
Pred. No. 4.2
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Pred. No. 2.2e-68
                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                   No. 4.2e-14;
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                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                    Length 261;
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                                                                                                                 -----FSPRI 50
                                                                                                                                                                                                                   87;
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A, Experimental source: strain MS11, variant 4.8
A; Note: the authors did not translate the sequence for the signal peptide
A; Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein
R; Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMHO J. 12, 641-650, 1993
A; Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms
A; Reference number: S36328; MUID:93178439
A; Accession: S36345
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C;Accession: S16611; S36345; S28624
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f A;Reference number: S16610; MUID:92114767
A;Accession: S16611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status F
F;24-260/Product: opacity protein opaJ #status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z18937; NID:g49333; PIDN:CAA79370.1; PID:g940799
A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
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F;165-211/Domain:
                                                                                                                                                                                                                                                                                                                    F;101-128/Region: hypervariable region HV1
F;134-148/Domain: transmembrane #status predicted <TM4>
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A; Residues: 24-260 < KUP>
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A;Variety: strain MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments) N; Alternate names: outer membrane protein opa58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S16611
                                                                                                             F;252-260/Domain:
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                                                                                                                                                                                              F;170-217/Region: hypervariable region HV2
F;212-224/Domain: transmembrane #status predicted
                                                                                                                                                                        228-236/Domain:
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 RVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 RYRF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 QNAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SDSFSQTSTGIGYLAGYSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGASAIYDFDTQSPVKPYLGARLSLN--RASVD------LGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKGNGNRTDLKAENQENGTFHAVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            semivariable region
                                                                                                                                                                                                                                                            extracellular #status predicted <EXT3>
                                                                                                                                                                                                                                                                                           transmembrane
                                                                                                             transmembrane #status predicted
                                                                                                                                                                        transmembrane
                                                                                                                                     extracellular
                     27.8%;
29.8%;
                                                                                                                                                                                                                                                                                     #status predicted
                                                                                                                                            #status
                                                                                                                                                                        #status
               Score 241;
Pred. No.
3 241; L.
Vo. 7e-14;
                                                                                                                                     predicted
                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KAPSTDFK------
                                                                                                                                                                        <TM6>
                                                                                                                                                                                                                                                                                                 <TM5>
                                                 Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <SIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
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120	Qy 47 SPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKL 80
	Db 97 SLLFAARAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKDKKSTVSDYFRNIRTHSI 156
. Ov 80	10 A
рь 6	27 7%: Score 240 5: DB 3: Israth
Qy	
Best Lo	249-295/Region: hypervariable region 290-302/Domain: transmembrane #status
Query N	224-289/Domain: 233-243/Domain:
F; 235-249	213-227/Domain: transmembrane #status predicted
F; 226-234	176-212/Domain: extracellular #status predicted
F; 168-215	156-164/Domain: transmembrane #statu
F;152-162	124-155/Domain: extracellular #statu 132-141/Region: semivariable region
F; 101-125	105-338/Product: opacity protein opaB #status predicted <mat> 115-123/Domain: transmembrane #status predicted <tm1></tm1></mat>
F; 88-94/I	C;Keywords: cell surface component; transmembrane protein F;1-13,14-104/Domain: signal sequence (fragments) #status predicted <sig></sig>
F; 50-60/1	Superfamily: opacity protein
F; 34-42/1 F; 43-74/1	C;Genetics:
F; 24-258,	; Note: expression of opacity proteins is regulated by the number of the proteins is required by the number of the proteins is required by the number of the proteins of the p
C; Keyword	S11, variant 4.8 nslate the sequence for the signal
A;Gene: (C;Superfa	
C;Genetic	Molecule t
	A; Receive number: Sibbly; MUID: 92114/6/ A; Recession: S16613
A; Experim A; Note: 1	A; Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A; Cross-	R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5. 1889-1901. 1991
A; Molecu.	ssion: S16613
A; Access	.y: strain MS11 04-Jun-1997 #sequence revision 17-Oct-1997 #tovt change
A;Title:	Neisseria gonorrhoea
Mol. Mici	v protein opaR precureor - Neisseria goporrhopa (ottain voit)
C; Access	RESULT 5
A; Variet	Db 244 NTR-FKTHEASLGVRYRF 260
opacity p	
RESULT 6 S16612	166 GEGITETVIEGKNIQUAHA
	106 OCCUPANTAL STATE OF THE STA
Db 33	116 G
Qy 17:	HTITAAAATITA
Db 27	Qy 80LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLG 115
Qy 11	Db 66 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKVNGNRTDRK 125
	Qy 48PRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 79
	Db 6 KRPSLLESSLLESSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSD 65
	QY 2 KKALATLIALALPAAALAEGASGEYVQADAAHAKASSSLGSAKGFS- 47
Db 15:	Matches 77; Conservative 25; Mismatches 68; Indels 88; Gaps 10;

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mental source: strain MS11, variant 4.8 the authors did not translate the sequence for the signal peptide expression of opacity proteins is regulated by the number of transits place the start codon in frame with the rest of the protein cs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.S.; Glbbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc riobiol. 5, 1899-1901, 1991

The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f nce number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 TQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7 SSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEEN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region: semivariable region

Domain: transmembrane #status predicted <TM2>
Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds: cell surface component; transmembrane protein 1-23/Domain: signal sequence (fragments) #status product: opacity protein opas #status predicted opacity protein opas #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein opaE precursor - Nelsseria gonorrhoeae (strain MS11) (fragments) s: Neisseria gonorrhoeae
y: strain MS11
y: strain MS11
104-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 YRF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD------LGG------ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain: transmembrane #status predicted <TM1>
Domain: extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amily: opacity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le type: DNA
es: 1-258 <BHA>
references: EMBL:X52369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ion: S16612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ----SDSFSQTSTGLGVLAGYSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                              //Domain: transmembrane #status predicted <TM7>
//Domain: extracellular #status predicted <EXT4
//Domain: transmembrane #status predicted <TM8>
NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGP 185
                                                ------LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD------LGG- 116
                                                                                                                                                                                                                KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 65
                                                                                                                                                                                                                                                                   KKALATLIALALPAAALAEG---ASGFYVQADAAHA-----KASSSLGSAK-----
                                                                                                      YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                                          -----GFSPRISAGYRINDLRFAVDYTRYK--NYKAPSTDFK-----
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                      27.6%;
                                                                                                                                                                                                                                                                                                                          ; Score 240; DB 2; Length 258; Pred. No. 8.5e-14; 24; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                          69; Indels 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted <SIG>
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translated repea
                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                          10;
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C; Superfamily: opacity protein
C; Keywords: cell surface component; transmembrane protein
F;1-11,12-24/Domain: signal sequence (fragments) #status
F;25-260/Product: opacity protein opac #status predicted
F;35-43/Domain: transmembrane #status predicted <TM1>
F;44-75/Domain: extracellular #status predicted <EXT1>
F;52-61/Region: semivariable region
F;76-84/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Variety: strain MS11
C; Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 16-Jul-1999
C; Accession: S16618; A24429; S36328; S28621
C; Accession: S16618; C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, R; Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
Mol. Microbiol. 5, 1889-1901, 1991
                                                                                                     F:89-95/Domain: transmembrane #status predicted <TM3>
F:96-134/Domain: extracellular #status predicted <EXT2>
F:102-129/Region: hypervariable region HV1
F:135-149/Domain: transmembrane #status predicted <TM4>
F:155-165/Domain: transmembrane #status predicted <TM5>
F:155-165/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1992
A;Reference number: $28617
A;Accession: $28621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: the authors translated the codon CCA for residue 32 as Thr A; Note: the authors did not translate the sequence for the signal peptide A; Note: expression of opacity proteins is regulated by the number of translate the start codon in frame with the rest of the protein of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opacity protein opaC precursor - Neisseria gonorrhoeae (strain MS11) (fragments) N;Alternate names: opacity protein VO; triosephosphate dehydrogenase C;Species: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
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F;166-211/Domain: extracellular #status predicted F;171-217/Region: hypervariable region HV2 F;212-224/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A: Residues: 25-260 <MEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 25-260 < KUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Variable opacity (CA; Reference number: S36328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F. EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 25-260 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variati
A; Reference number: A90887; MUID:87002493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stern, A.; Brc
Cell 47, 61-71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain MS11, variant 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Meyer, T.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S36328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: this protein is synthesized as a precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: X52370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S16618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-FKTHEASLGVRYRF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTPTVYPGKNTQDAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-260 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown, M.; Nickel, P.; Meyer, T.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opacity protein
ll surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Opa) outer membrane proteins account 
3; MUID:93178439
   predicted <TM6>
                                                                              <EXT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        however,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
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F;228-236/Domain: transmembrane *status predicted F;237-251/Domain: extracellular *status predicted F;252-260/Domain: transmembrane *status predicted
                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-237/Product: opacity protein opa57 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: $36328; A; Accession: $36343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Kupsch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment) N; Alternate names: outer membrane protein opa57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
S36343
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                                                                                  F;214-228/Domain:
F;229-237/Domain:
                                                                                                                                        F;147-194/Region: hypervariable F;189-201/Domain: transmembrane
                                                                                                                                                                                                                            F;78-105/Region: hypervariable region HVI F;111-125/Domain: transmembrane #status p
                                                                                                                                                                                                                                                                                         F;52-60/Domain: transmembrane #status predicted F;65-71/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                  F; 28-37/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of repeats place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: expression of opacity proteins is regulated by the number of translated of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z18935; NID:g49331; PIDN:CAA79368.1; PID:g940797
A;Experimental source: strain MS11, variant F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms A; Reference number: S36328; MUID:93178439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kupsch, E.M.; Knepper, EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date:
                                                                                                                         F;205-213/Domain:
                                                                                                                                                                                     F;142-188/Domain: extracellular #status predicted <EXT3>
                                                                                                                                                                                                         F;131-141/Domain: transmembrane
                                                                                                                                                                                                                                                                     F;72-110/Domain:
                                                                                                                                                                                                                                                                                                                                                   F;20-51/Domain:
                                                                                                                                                                                                                                                                                                                                                                      F;11-19/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: opa57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-237 < KUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 EASLGVRYRF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 SFHAVSSLGLSAIYDFQINDKFKPYIGARVAYGHVRHSIDSTKKITGLLTTSTPGIMSGV 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 SSILFSSAAQAASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRT 73
                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
sion: S36343; S28626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ATLIALALPAAALAEGASGFYVQADAAHA-----KASSSLGSAKGFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKVLRTPGAHRESDSIRR--VGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --FKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                 Similarity
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Conservative
                                                                                                                                                                                                                                                                     extracellular #status predicted <EXT2>
                                                                                                   extracellular
                                                                                                                           transmembrane
                                                                                  transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.; Kuroki, T.;
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29.2%;
                     27.6%;
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  24;
                                                                                                                         #status predicted
                                                                                  #status
                                                                                                                                          #status predicted
                                                                                                                                                                  region HV2
                                                                                                     #status predicted
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                     Pred. No.
                                         Score 239.5;
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  59;
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    85;
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  Gaps
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F;99-131/Domain: extracellular *status predicted <EXT2>F;101-126/Region: hypervariable region HVI
F;132-146/Domain: transmembrane *status predicted <TM4>F;152-162/Domain: transmembrane *status predicted <TM5>F;163-208/Domain: extracellular *status predicted <EXT3>F;168-214/Region: hypervariable region HV2
F;209-221/Domain: transmembrane *status predicted <TM6>F;225-33/Domain: transmembrane *status predicted <TM7>F;234-248/Domain: transmembrane *status predicted <TM7>F;234-248/Domain: extracellular *st
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A; Residues: 1-257 cBHA>
A; Cross-references: EMBL: X52368
A; Experimental source: strain MS11, variant 4.8
A; Experimental source: strain MS11, variant 4.8
A; Experimental source: strain HS11, variant 4.8
A; Note: the authors translated the codon ACC for residue 206 as Ala and TAT for residue A; Note: the authors did not translate the sequence for the signal peptide
A; Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
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F:24-257/Product: opacity protein opaF #status predicted
F:34-42/Domain: transmembrane #status predicted <TMl>
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C;Superfamily: op
C;Keywords: cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;75-83/Domain: transmembrane #status predicted <TM2>
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F:43-74/Domain: extracellular #status predicted <EXT1>
F:51-60/Region: semivariable region
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A;Accession: S16614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S16614
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
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                                                                                                 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                                                                                                                                                                                                       KKALATLIALALPAAALAEG---ASGFYYQADAAHA-----KASSSLGSAK------ 44
                        ------LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD------LGG 116
                                                                                                                                                                                                                                                      KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGVRYRF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNTQDAH 180
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                                                                                                                                                                              --GFSPRISAGYRINDLRFAVDYTRYK--NYKAPSTDFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane #status
27.6%;
29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 239.5;
Pred. No. 9.3
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
                                                                                                                                                                                                                                                                                                                                                                                                            9.3e-14;
ches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMI3>
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;171-217/Domain: extracellular #status predicted <EXT3:
F;176-223/Region: hypervariable region HV2
F;218-230/Domain: transmembrane #status predicted <TM6>
F;234-242/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;95-139/Domain: extracellular #status predicted <EXT2>F;101-134/Region: hypervariable region HV1
F;140-154/Domain: transmembrane #status predicted <TM4>F;160-170/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;88-94/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;51-60/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: opaD
C; Superfamily: opacity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain MS11, variant 4.8 A;Note: the authors did not translate the sequence for the signal peptide A;Note: expression of opacity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;75-83/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-266 <BHA>
A;Cross-references: EMBL:X52372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 5, 1889-1901, 1991 And Notice of Neisseria gonorrhoeae strain MS11 are encoded by a f A;Reference number: S16610; MUID:92114767 A;Accession: S16616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opacity protein opaD precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        벙
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                                                        186
                                                                                                         108
                                                                                                                                                            126
153 GKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                              66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGG 185
                                                                                                                                                                                                                                                                                                                 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                  2 KKALATLIALALPAAALAEG---ASGFYYQADAAHA-------KASSSLGS- 42
                                           AVTTYPQNAASSVTTNAPIRKLPHHESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNW
                                                                                                                                         NIKTRKTEHRENGTFHAASSLGLSAVYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETI 185
                                                                                                                                                                                                                                              YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIKELLRNDNANSGGSHL 125
                                                                                                                                                                                                NYKAPSTDFK-----LYSIGASAIYDFDTQSPVKPYLGARLSL----
                                                                                                                                                                                                                                                                                                      ----AKGFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                                  KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTAPKKAQLSTVSD 65
                                                                                      -----NRASV------DLGGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 266;
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C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
C;Keywords: cell surface component; transmembrane protein
F;1213,14-21/Domain: signal sequence (fragments) #status predicted <MAN
F;22-258/Product: opacity protein-related protein OPM1 #status predicted <MAN
F;33-41/Domain: transmembrane #status predicted <MXTI>
F;42-73/Domain: extracellular #status predicted <MXYI
F;0-59/Region: semivariable region
F;50-59/Region: semivariable region
F;74-82/Domain: transmembrane #status predicted <MX3>
F;87-93/Domain: extracellular #status predicted <MXYI
F;100-124/Region: hypervariable region HV1
F;100-1144/Domain: transmembrane #status predicted <MX4>
F;150-160/Domain: transmembrane #status predicted <MX5>
F;161-209/Domain: extracellular #status predicted <MX7>
F;162-215/Region: hypervariable region HV2
F;162-225/Domain: transmembrane #status predicted <MX7>
F;162-225/Domain: transmembrane #status predicted <MX7>
F;163-225/Domain: transmembrane #status predicted <MX7>
F;164-225/Domain: transmembrane #status predicted <MX7>
F;165-215/Region: hypervariable region HV2
F;210-225/Domain: transmembrane #status predicted <MX7>
F;165-215/Region: hypervariable region HV2
F;210-225/Domain: transmembrane #status predicted <MX7>
F;210-225/Domain: transmembrane #status predicted <MX7
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A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
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A;Variety: strain C1938
C;Date: 19-Mar;1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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Mol. Microbiol. 1, 5-12, 1987
A;Title: Common mechanism controlling phase and antigenic variation in pathogenic neiss
                            RESULT 12
S20043
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opacity protein
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Residues: 1-258 <STE>
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250-258/Domain:
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                                                                                                                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 SSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPKGGTPAGGPVIK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LFSSAAQAASEDGSRSPYYVQADLAYAAERITHNYPEPTGADKDKISTVSDYFRNIRAHS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 IHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKTEHQGNGSFHAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 FSPRISAGYRINDLRFAVDYTRYK------ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LIALALPAAALAEGASGFYVQADAAHA-----
                                                                                                                                                                                                                                                                                                               TDPSKPPYHESHSISSIGIGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEASL
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                                                                                                                                                                         GMRYRF
                                                                                                                                                                                                                                                                                                                                                                                -----DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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precursor (clone pFLOB1700) - Neisseria meningitidis (strain FAM18)
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28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 237; Db 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <EXT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ASVDLGGS----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-19/Domain: signal sequence (fragment) #status predicted <SIG>F;20-254/Product: opacity protein opaB #status predicted <MAT>F;31-39/Domain: transmembrane #status predicted <TM1>F;40-69/Domain: extracellular #status predicted <EXTI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X63108
A;Experimental source: strain FAM18; clone pFLOB1700
A;Experimental source: strain FAM18; clone pFLOB1700
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A;Note: only a part of the translation is shown
A;Note: expression of opacity proteins is regulated by the number of translated repeated to the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: outer membrane protein class 5
C;Species: Neisserla meningitidis
A;Variety: strain FAM18
C;Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Aho, E.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.
Mol. Microbiol. 5, 1429-1437, 1991
A;Title: Characterization of the opa (class 5) gene family of Neisseria meningitidis.
A;Reference number: S16286; MUID:92157869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S20043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;158-205/Domain: extracellular #status predicted <EXT3>F;163-211/Region: hypervariable region HV2
F;206-218/Domain: transmembrane #status predicted <TM5>F;222-230/Domain: transmembrane #status predicted <TM7>F;231-245/Domain: extracellular #status predicted <EXT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;48-55/Region: F;70-78/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;96-121/Region: hypervariable region HV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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251 RYHF 254
                                                      171 RVKF 174
                                                                                                             192
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                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LFSSAAQAASEDGSRSPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                          STQNAYHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM
                                                                                                                                                                                                                     SLGLSAIYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVVTLTHGGADTKPTIYNGE 191
                                                                                                                                                                                                                                                                            SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL-------GGSD------
                                                                                                                                                                                                                                                                                                                             PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS 131
                                                                                                                                                                                                                                                                                                                                                                                    PRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIALALPAAALAEGASGFYVQADAAHA------KASSSLGS------AKGFS 47
                                                                                                                                                              -----SFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-254 <AHO>
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transmembrane #status predicted <TM3>
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28.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                             -KAPSTDFKLY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fr C:Species: Neisseria gonorrhoeae A;Variety: strain F62-SF C;Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998 C:Accession: S04380; S15504 R;Palmer, L.; Brooks, G.F.; Falkow, S.

RESULT 13

Mol. Microbiol. 3, 663-671, 1989

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          opacity protein P.IIc
                                           KONH2C
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F:162-172/Domain: transmembrane #status predicted <TM5>
F:173-221/Domain: extracellular #status predicted <EXT3-
F:178-227/Region: hypervariable region HV2
F:222-334/Domain: transmembrane #status predicted <TM6>
F:222-334/Domain: transmembrane #status predicted <TM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: opaE1
C;Superfamily: opacity protein
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status F;24-270/Product; opacity protein opaK #status predicted <F;34-42/Domain: transmembrane #status predicted <TML>
F;34-42/Domain: extracellular #status predicted <TML>
F;43-75/Domain: extracellular #status predicted <EXTI>
F;51-61/Region: semivariable region
F;51-61/Region: semivariable region
                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain MS11A
A; Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1 A; Note: the authors did not translate the sequence of the signal peptide A; Note: expression of opacity proteins is regulated by the number of translate the start codon in frame with the rest of the protein R; Taha, M.K.; So, M.; Seifert, H.S.; Billyard, E.; Marchal, C. EMBO J. 7, 4367-4378, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;102-136/Region: hypervariable region HV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: S02017; MUID:89210824
A;Accession: S16504
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X13965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 259-270 <TAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X15780
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A; Residues: 1-270 < PAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238-246/Domain:
                                                                                                                                      246 YHNWGRLENTR-FKTHEASLGVRYRF 270
                                                                                                                                                                                                                                 186 TEIVTTYPKEQNVAPSPIPGAPTKKPAHHESRSISSLGFGAVAGVGIDITPNLTLDAGYR 245
                                                                                                                                                                                                                                                                                                                                    126 HLNIQTQKTEHQENGTFHAASSLGLSTIYDFDTGSRFKPYIGARVAYGHVRHQVRSVEQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                         66 DYFRNIRTHSVHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELGRNDNSASGVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 GF-----SPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                                                                           70 --NYKAPSTDFK-----LYSIGASAIYDFDTQSPVKPYLGARLSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KKPSLLFSSLLFSSAAQAAGEGNGRGPYVQADLAYAYEHITHDYPKPTGAKKGTTISTVS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KKALATLIALALPAAALAEG---ASGFYYQADAAH-----AKASSSLGSAK 44
                                                                                                                                                                                        YNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                  ------NRASVDLGGS------DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYR 148
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extracellular
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precursor - Neisseria gonorrhoeae (strain JS3) (fragments)
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27.4%;
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Pred. No. 2e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245-259/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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F;260-268/Domain: transmembrane #status predicted
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F;88-94/Domain: transmembrane #status predicted <TM3>
F;95-140/Domain: extracellular #status predicted <EXT2>
F;101-135/Region: hypervariable region HV1
F;101-155/Domain: transmembrane #status predicted <TM4>
F;101-171/Domain: transmembrane #status predicted <TM5>
F;101-171/Domain: extracellular #status predicted <EXT3>
F;101-171/Domain: extracellular #status predicted <EXT3>
F;107-205/Region: hypervariable region HV2
F;202-232/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-33/Domain: signal sequence (fragments) #status predicted <SIG>
F;24-268/Product: opacity protein P.IC #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: 241-val was also found
A;Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein
R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
Infect. Immun. 55, 2026-2031, 1987
A;Title: Antigenic and structural differences among six proteins II expressed by a si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;34-42/Domain: transmembrane #status predicted <TMl>F;43-74/Domain: extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S16360; MUID:87306843
A;Accession: S16360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Microbiol. 2, 797-806, 1988
A; Title: Three copies of a single protein II-encoding sequence in the genome of Neiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S03095; MUID:89096501
A;Accession: S03095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain JS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X12625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S03095; S16360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236-244/Domain: transmembrane
                                                                                                         193 SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN 252
                                                                                                                                                                  115 ---GGSDSFSQ------TSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNT 157
                                                                                                                                                                                                                            133 TEHQENGTFHAVSSLGLSTIYDFDTGSRFKPYIGMRVAYGHVRHQVRSVEQETEIITTYP 192
                                                            158 VKNVRSGELSAGVRVKF 174
253 TR-FKTHEASLGMRYRF 268
                                                                                                                                                                                                                                                                                     76 TDFK------LYSIGASAIYDFDTQSPVKPYLGARLSLNRA-----SVDL-----
                                                                                                                                                                                                                                                                                                                                                  73 HSVHPRVSVGYDFGSWRIAADYARYRKWNNNKYSVSIKELLRNDNSASGVRGHLNIQTQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                     45 -GFSPRISAGYRINDLRFAVDYTRYK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ATLIALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAK-------44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLLFSSAARAASEDGGRGPYVQADLAYAAERITHDYPKPTGTGKNKISTVSDYFRNIRT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.1%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 235.5; DB 1;
Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                  -----NYKAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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RESULT 15

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opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
N;Alternate names: cell invasion protein opaH
C:Species: Neisseria gonorrhoeae
A;Variety: isolate 15063G
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S72343
R;Maldbeser, L.S.: Atioka R S. Marr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U13708; NID:g535357; PIDN:AAA74082.1; PID:g535358
A;Experimental source: isolate 150636
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A;Note: expression of opacity proteins is regulated by the number of translated repeat
A;Note: expression of opacity proteins is regulated by the number of translated repeat
Of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;99-107/Domain: transmembrane *status predicted <TM3>
F;112-118/Domain: transmembrane #status predicted <EXT2>
F;119-155/Domain: extracellular #status predicted <EXT2>
F;119-155/Domain: hypervariable region HV1
F:125-150/Region: hypervariable #status predicted <TM4>
F:156-170/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-48/Domain: signal sequence *status predicted <SIG>
F;49-283/Product: opacity protein opaH *status predicted <MAT>
F;58-66/Domain: transmembrane *status predicted <TM1>
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R;Waldbeser, L.S.; Ajioka, R.S.; Merz, A.J.; Puaoi, D.; Lin, L.; Thomas, M.; So, M. Mol. Microbiol. 13, 919-928, 1994
Mol. Microbiol. 13, 919-928, 1994
A;Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in A;Reference number: S72343; MUID:95115561
A;Accession: S72343
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A; Residues: 1-283 <WAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;176-186/Domain: transmembrane #status predicted <PM5>F;187-234/Domain: extracellular #status predicted <EXT3>F;187-240/Region: hypervariable region HV2
F;235-247/Domain: transmembrane #status predicted <PM6>F;235-247/Domain: transmembrane #status predicted <PM5>F;235-247/Domain: tran
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Search completed: October 28, 2002, 16:03:36 Job time: 13.4821 secs
                                                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       280 RYRF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 RVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 KTQDAHQESNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGM 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 ----GGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 PRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIERVQEAHSNRIDLKAENQENGTFHAVS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL------ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 SLLSAAQAASEAMRGPYVQADLAFAAERITHDYPEPTGTKKGTISTVSDYFRNIRTHSVH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAKG-----FS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKILTSFYGVATKPTTYDIGP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <TM7>
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OM protein - protein search, using sw model GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

October 28, 2002, 15:55:44; Search time 6.98996 Seconds (without alignments) 963.840 Million cell updates/sec

Title:
Perfect score: Sequence: US-09-684-883-6 868 1 MKKALATLIALALPAAALAE......VNTVKNVRSGELSAGVRVKF 174

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ີ ວັ	0	Query Match L	Length :	DВ	ID	Description
	239.5	27.6	237	- :	OPAK_NEIGO	Q04880 neisseria q
N			260	_	1 1	170 neisser
ω	235.5	27.1	270	٢	OMPC_NEIGO	neisseria
4	234		236	ب سا	OPAC_NEIGO	neisseria
Ç	231.5		234	\vdash	OPAB_NEIGO	neisseria
o.	ω		237	\vdash	OPAJ_NEIGO	ne :
7	231	•	234	٢	OPAE_NEIGO	neisseria
80	231	•	234	Н	OPAF_NEIGO	neisseria
. 6	230	•	233	ب	OP67_NEIGO	4 neisseria
10	225	•	234	ш	OP28_NEIGO	neisseria
11	225	•	234	_	OP65_NEIGO	
12	225	٠	238	-	OP66_NEIGO	neisseria
1.5		٠	238	Н	OPAH_NEIGO	neisseria
14	223.5	٠	243	-	OPAD_NEIGO	neisseria
15	223	٠	244	-	OPAI_NEIGO	neisseria
16	220	٠	178	Н	YE57_HAEIN	haemophilu
10	219	٠	238		OP68_NEIGO	neisseria
10	2014	•	239	۰ ۲	OPAA_NEIGO	neisseria
) L	177.5	•	24/	۰ ۲		Q04875 neisseria g
2 6	176	•	121	-	OPA_HAEIN	haemophilu
2	135	15.6	170	-	OPR3_NEIMC	neisseria
22	122.5	•	70	Н	Y414_HAEIN	haemophilu
. 23	113		182	₽	AIL_YERPS	7
24	100	11.5	353	Н	OM52_HAEIN	P38368 haemophilus
) N		11.4	ω 5 3	Н	OM51_HAEIN	
0 0	98.5	11.3	350	Ψ	OMPA_SALTY	P02936 salmonella
27	8 6	•	521	μ.	TSAS_RICTS	P37917 rickettsia
0 00	97	11.2	213	ч	OM25_BRUAB	Q44664 brucella ab
200	96	11.1	178	Н	AIL_YEREN	
30	9	11.1	212	μ	OMPW_ECOLI	escherich
31	93.5	10.8	341	Н	OMPU_VIBCH	
32	·	10.8	428	۳	OM47_PASMU	ω
33	93	10.7	359	1	OM53_HAEIN	P45996 haemophilus

4.4	432	40 41	3 3 9 8	36	ωω 4 70
82	83.5 83	84 4	87 84.5	87 87	88.5
9.4	, , , , ,	9.7 9.7	10.0 9.7	10.0	10.3
172	350 201	511 511	350 995	213 349	213 346
					1
OMPX_ENTCL	OMPA_ENTAE OM25_BRUOV	INO1_ARATH INO1_PHAVU	PORF_PSEAE YIQ9_YEAST	OM25_BRUME OMPA_BUCAI	OM25_BRUSU OMPA_ECOLI
045110 brucella ca P25253 enterobacte	P09146 enterobacte Q45335 brucella ov		P13794 pseudomonas P40442 saccharomyc		Q45689 brucella su P02934 escherichia

ALIGNMENTS

Query Match 27.6%; Score 239.5; DB 1; Length 237; Best Local Similarity 30.0%; Pred. No. 1.6e-14; Matches 72; Conservative 24; Mismatches 59; Indels 85; Gaps Qy 17 ALAEGASGEYVQADAAHA	DR EMBL; Z18935; CAA79368.1; DR PIR; S28626; S28626. DR InterPro; IPR003394; Opacity. DR Pfam; PF02462; Opacity; 1. KW Outer membrane; Multigene family; Signal. FT NON_TER 1 1 POTENTIAL. FT SIGNAL <1 1 POTENTIAL. FT CHAIN 2 >237 OPACITY PROTEIN OPAS7. FT NON_TER 237 237 SQ SEQUENCE 237 AA; 26703 MW; F8B1A0FB5C7EECAD CRC64;	SWISS-PROT entry is copyright. It is produced through a colen the Swiss Institute of Bioinformatics and the EMBL ou uropean Bioinformatics Institute. There are no restrictic by non-profit institutions as long as its content is ried and this statement is not removed. Usage by and for les requires a license agreement (See http://www.isb-sib.ch.nd an email to license@isb-sib.ch).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=MSII / F3; MEDLINE=93178439; PubMed=8440254; Kupsch EM., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account for the tropisms displayed by Neisseria gonorrhoeae for human leukocytes epithelial cells."; EMBO J. 12:641-650(1993). -!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPP. PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO IN VARIATION. -I- SUBCELLULAR LOCATION: Outer membrane.	RESULT 1 OPAK_NEIGO STANDARD; PRT; 237 AA. AC Q04880; DT 01-OCT-1993 (Rel. 27, Created) DT 01-OCT-1995 (Rel. 32, Last sequence update) DT 01-NOV-1995 (Rel. 32, Last annotation update) DE Opacity protein OPA57 precursor (Fragment). GN OPAK. OS Neisseria gonoxrhoeae. OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria OX NCBI_TaxID=485; RN [11]
; Ga SAGY SVGY IGAS LGLS		h a collaboration EMBL outstation trictions on its is in no way nd for commercial rsib.ch/announce/	the cell ytes and OPA TO PHASE	eisseria.

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P10170;
01-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogenic neisseriae."
Mol. Microbiol. 1:5-12(
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Bacteria; Proteobacteria; beta subdivision;
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16-OCT-2001
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SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
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                              VKNVRSGELSAGVRVKF 174
                                                                                                                       EHQGNGSFHATSSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPK 184
                                                                                                                                                      DFK-----LYSIGASAIYDFDTQSPVKPYLGARLSLNR------ASVDL 114
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                                                           GGTPAGGPVIKTDPSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLEN 244
                                                                                            GGS---
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                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                         260 AA; 28936 MW;
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(Rel. 10, Last sequence up
(Rel. 40, Last annotation
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No. 2.4e-14;
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01-NOV-1990 (Rel. 16,
01-FEB-1994 (Rel. 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93178439; PubMed-8440254; Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; Wariable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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Pfam; PF02462; Opacity; 1.
Outer membrane; Multigene family; Signal.
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EMBL; Z18927; CAA79360.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-MS11 / VO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=485;
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                   DFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENGSFHAVSSLGLS
     AIYDFDTQSPVKPYLGARLSLN--RASVD-
                                                                                                                                                                                                                ALAEGASGFYVQADAAHA-----KASSSLGSAKGFS------PRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S36328; S36328.
                                                                                                                                                               ASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRTHSIHPRVSVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S28621;
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                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         236
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         AA;
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1. 32, Last annotation update)
OPASO precursor (OPA30) (VO) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                               >236
                                                                                                                                                                                                                                                                                                                                                                                   26685 MW; 68DC237692183398 CRC64;
                                                                                                                                                                                                                                                                                                   27.0%; Score 234; DB 1 29.7%; Pred. No. 5e-14;
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OPACITY PROTEIN OPA50.
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                                                                                                         KNYKAPSTD----FKLYSIGAS
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Indels
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Best Local
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NON_TER
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MEDLINE-93178439; PubMed-8440254;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

"Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.",

embo J. 12:641-650(1993).

-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Opacity protein OPA51 precursor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane; Multigene family; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae
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                                                                                                               122

    !- SUBCELLULAR LOCATION: Outer membrane.

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                                                                                                                                                                                                                                                                                                                              N
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$36329; $36329.
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SIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                                                                                                                   SEGNGRGPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYD 61
                                               SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                    DFKLNGKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEENTQNAHHQSN
                                                                                                                                                            DFDTQSPVKPYLGARLSLN--RASVD---
                                                                                                                                                                                                               FGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTENQENGTFHAVSSLGLSAVY
                                                                                                                                                                                                                                                                 INDLRFAVDYTRYK--NYKAPSTDFK----------LYSIGASAIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9FFE5B5DABBA96CA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 234;
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RESULT 7
OPAE_NEIGO
ID OPAE_N
AC Q04878
DT 01-OCT
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Best Local :
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NON_TER
OPAE_NEIGO STANDARD;
Q04878;
01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z18937; CAA79370.1; -. 
PIR; S28624; S28624; S28624; Clarer 
InterPro; IPR003394; Opacity. 
Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelial cells.";
embo J. 12:641-650(1993).
-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OF PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer mebrane proteins account for the cell
"Variable opacity (Opa) outer for human lenkowytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPAJ_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ptam; PFU2462; Opacity; 1.
Outer membrane; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tropisms displayed by Neisseria gonorrhoeae for human leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                         R--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                         QTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                            NDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNTQDAHRESDSIR
                                                                                                                                                                                                                            QSPVKPYLGARLSLN--RASVD------LGG------SDSFS
                                                                                                                                                                                                                                                             AADYARYRKWNNNKYSVSIKELLRNKVNGNRTDRKTENQENGTFHAVSSLGLSAVYDFKL 127
                                                                                                                                                                                                                                                                                                 AVDYTRYKNY------KAPSTDFK------LYSIGASAIYDFDT
                                                                                                                                                                                                                                                                                                                                 GPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI 67
                                                                                                                                                                                                                                                                                                                                                                                                    70;
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
237 AA;
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>237
237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26855 MW; B165033B2CBD6A53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 26.7%; Score 231.5; 30.0%; Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPACITY PROTEIN OPA58.
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Q04879;
01-0CT-1993 (Rel. 27, C
01-0CT-1993 (Rel. 27, I
01-NOV-1995 (Rel. 32, I
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"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells.";
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01-NOV-1995 (Rel. 32,
Opacity protein OPA55
OPAE.
                          Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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MEDLINE=93178439; PubMed=8440254;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
                                                                                                          Opacity protein
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OF PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO
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Last annotation updat
                             beta subdivision; Neisseriaceae; Neisseria.
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Best Local
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 MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
                                                                                                                                                                                                                                                        LNEIGO
                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA67 precursor (Fragment).
epithelial cells.";
                                                                                                                                Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                   Q05034;
01-OCT-1993 (Rel.
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                                                                          STRAIN-VP
                                                                                     SEQUENCE FROM N.A.
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MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cropisms displayed by Neisseria gonorrhoeae for human leukocytes
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Pfam; PF02462; Opacity; 1.
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SEQUENCE FROM N.A.
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS
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                                                                                                                              beta subdivision; Neisseriaceae;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                 antigenic variation.";
Cell 47:61-71(1986).
-!- FUNCTION: IMPLICATI
                                                                                                                                                                     MEDIJINE-87002493; PubMed=3093085; MEDIJINE-87002493; PubMed=3093085; Stern A., Brown M., Nickel P., Meyer T.F. Obacity genes in Neisseria gonorrhoeae:
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01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
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SEQUENCE
                                                                                                                                                                                                                                                                  Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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                                                                                -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=485
                                                                                                                                                                                                                                                                                                  Opacity protein V28 precursor (Fragment).
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-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
-PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
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                                                                                                                PROTEINS ARE IMPLICATED
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65; Conserva
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                                                                                                                                                                                                                               epithelial cells.";
EMBO J. 12:641-650(1993).
-i-FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                          MEDLINE=93178439; PubMed=8440254; Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Opacity protein OPA65 precursor (Fragment).
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Pfam; PF02462; Opacity; 1.
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                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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         EMBL; Z18940; CAA79373.1; -. PIR; S28617; S28617. InterPro; IPR003394; Opacity.
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                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
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01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
Opacity protein OPA66 precursor (Fragment).
                                                                                     InterPro; IPR003394; Opacity.
Pfam; PF02462; Opacity; 1.
                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                     epithelial cells.";
EMBO J. 12:641-650(1993).
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account fo
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=VP1
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                                                                         Outer membrane; Multigene family; Signal
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                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                          FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Outer membrane.
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                                                                                                                                  Z18941; CAA79374.1; -.
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                                 OPACITY PROTEIN OPA66.
                                                POTENTIAL
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    B6E38AF1585263AA CRC64;
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OPAH_NEIGO
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                           EMBL; Z18939; CAA79372.1; -. EMBL; X60711; CAA43121.1; -. PIR; S28631; S28631.
                                                                                                                                                                            modified and this statement entities requires a license
                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The opacity proteins of Neisseria gonorrho
encoded by a family of 11 complete genes.",
Mol. Microbiol. 5:1889-1901(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92114767; PubMed=1815562;
Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhat K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92261323; PubMed=1584024;
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SEQUENCE FROM N.A.
TN=MS11 / V18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account fo tropisms displayed by Neisseria gonorrhoeae for human leuk epithelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Opacity protein OPA60 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93178439; PubMed=8440254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 NDKFKPYIGARVAYGHVRHSIDSTKKTTEELTTAGARGTDPTVSSPYKNTQDAHQESNSI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 TSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t K.S., G1bbs C.P., Barrera O., Morrison S.G., Jaehnig F., rn S., Kupsch E.-M., Meyer T.F., Swanson J.;
Microbiol. 6:1073-1076(1992).
FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
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                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEINS ARE IMPLICATED IN PATHOGENESIS
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IPR003394; Opacity
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Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                     is not removed.
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF ADHERENCE FUNCTIONS. OPA
N PATHOGENESIS AND ARE SUBJECT TO PHASE
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smatches 58;
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RESULT 14
OPAD_NEIGO
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           STRAIN-MS11 / F3;

MEDLINE-93178439; PubMed-8440254;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

"Variable opacity (Opa) outer membrane proteins account for the cropisms displayed by Neisseria gonorrhoeae for human leukocytes epithelial cells.",

EMBO J. 12:641-650(1993).

-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q04883;
01-OCT-1993
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    CHAIN
                                                                               EMBL; Z18938; CAA79371.1; -. PIR; S28629; S28629.
                                     Outer membrane; Multigene family; Signal.
                                                       Pfam;
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PF02462; Opacity; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               27, Created)
27, Last sequences 32, Last annotations.
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OPACITY PROTEIN OPA59
             POTENTIAL.
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Pred. No. 3.2e-13;
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SED -> MLKA (IN MS11 /
V -> M (IN MS11 / V18)
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Query Match
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Q04877;
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01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
0pacity protein OPA54 precursor (Fragment).
                                                                                                                                                                         EMBL; Z18931; CAA79364.1; -.
EMBL; Z18932; CAA79365.1; -.
PIR; S28622; S28622.
PIR; S28618; S28618.
PIR; S36332; S36332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the cell
"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - 1 - F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Outer membrane.
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                                   SEQUENCE
                                                                                           SIGNAL
                                                                                                                            Outer membrane;
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                                                         NON_TER
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
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243 AA;
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                                                                                                                            Multigene family; Signal.
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27414 MW; 5930C73917436041 CRC64;
                                     27488 MW; 968AB8603D961DD8 CRC64;
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Last annotation update)
   25.7%; Score 223; DB 1; Length 244;
                                                                          OPACITY PROTEIN OPA54.
                                                                                            POTENTIAL.
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188 HESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 244
                                     117
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                                                                                                                                            68 AADYARYRKWNNNKYSVNIKELLRNDNANSGGNKHLNIKTRKTEHRENGTFHAASSLGLS
                                                                                                                                                                                  62 AVDYTRYK-----LYSIGAS
                                                                                                                                                                                                                                                    24 GFYYQADAAHA-----KASSSLGSAK-------GFSPRISAGYRINDLRF
                                                                                                                                                                                                                  8 GPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRI
                                    SDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
                                                                        AVYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETIAVTTYPQNAASSVTTNAPIRKLPH 187
                                                                                                                                                                                                                                                                                        Conservative
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Search completed: October 28, 2002, 16:01:12 Job time: 7.98996 secs

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Result
No.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   Score
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868
1 MKKALATLIALALPAAALAE.....VNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562222 seqs, 172994929 residues
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Copyright (c) 1993 - 2002 Compugen Ltd.
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   16 P95372
2 O9RP16
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2 Q51124
16 Q9CM19
2 Q9AE80
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P95372 neisseria m
Q9rp16 neisseria m
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033389	031175	007278	031172	Q9k4t8	Q9k4t7	030752	007273	Q9k4t6	Q9r9a8	Q9r9a9	030753	Q9k4t5	Q51303	Q51013	007925	Q509 4 3	007912	Q9k4t3	033388	007274	007287	050929	Q9rqv4	Q9r3p5	N	N	Q9k4t4	Q9r9a7
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ALIGNMENTS

RESULT 1 P95372 PPELIMINARY; PRT; 174 AA. AC P95372; O1-MAY-1997 (TIEMBLIFEL 03, Created) DT 01-MAY-1997 (TIEMBLIFEL 03, Last sequence update) DT 01-MAY-1997 (TIEMBLIFEL 03, Last annotation update) DT 01-MAY-1997 (TIEMBLIFEL 19, Last annotation update) DE COUTER MEMBRANE PROTEIN PRECURSOR. No Security Protection A. Response of the subdivision; Neisseriaceae; Neisseria Neisseria meningitidis (serogroup A). Response from N.A. Response from N.A. Response from N.A. Response from N.A. Response from D., Cadleux N., Hamel J., Rioux C., Brodeur B.R.; RN MEDLINE-20222556; Pubbed-10761919; RN MEDLINE-2022256; RN MEDLINE-2022256; RN MEDLINE-2022256; RN MEDLINE-2022
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RESULT 3
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AC Q9R2A
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Best Local Similarity
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01-MAY-2000
01-JUN-2001
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Q9R2R1;
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01-MAY-2000
01-JUN-2001
                                                                                                                                      NSPA.
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"Differences in Surface Expression of Neisserial Surface Protein among Neisseria meningitidis Group B strains.";

Infect. Immun. 0:0-0(1999).

EMBL; AF175681; AAD53284.1; -
InterPro; IPR003394; Opacity.

Pfam; PF02462; Opacity.

Pfam; PF02462; Opacity; 1

SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;
SEQUENCE FROM N.A. STRAIN=M136, AND BZ232;
                                                                                        Neisseria meningitidis.
Bacteria; Proteobacteria;
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                                                                  NCBI_TaxID=487;
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Pred. No. 1.8e-64;
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Q9RP18;
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"Differences in Surface Expression of Neisserial among Neisseria meningitidis Group B strains.";
Infect. Immun. 0:0-0(1999).
EMBL; AF175679; AAD53282.1; -.
EMBL; AF175677; AAD53280.1; -.
InterPro; IPR003394; Opacity.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                               SEQUENCE
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EMBL; AF175676; AAD53279.1; -.
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Bacteria; Proteobacteria;
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Pfam; PF02462; Opacity; 1.
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                                                                                                                                                                                                                                                                                             174 AA; 18357 MW;
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Pred. No. 5.5e-64;
1; Mismatches 1
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Pred. No. 3.8e-64;
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                                                                                                                                                                                                                       P96943;
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-JUN-2001 (TrEMBLrel. 17,
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EMBL; AF175678; AAD53281.1; --
EMBL; AE002420; AAF41081.1; --
                   Martin D., Cadieux N., Hamel J.,
                              MEDLINE=97149429; PubMed=8996237;
                                                     STRAIN-608B;
                                                                                                               Bacteria;
                                                                                                                           Neisseria meningitidis
                                                                                                                                                          OUTER MEMBRANE PROTEIN PRECURSOR.
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Neisseria meningitidis (serogroup B).
Neisseria; Proteobacteria; beta subdivision; Neisseriaceae;
*Costimulation of T cell activation by integrin-associated
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"Differences in Surface Expression of Neisserial Surface among Neisseria meningitidis Group B strains.";
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                                                                                                                                                                                                                                                                                                                             SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                        FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                        FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASYDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKKALATLIALAAAALAEGASGEYYQADAAHAKASSSLGSAKGESPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                             SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMB0663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immun.
                                                                                                              Proteobacteria;
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                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18397 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.8%; Score 858; 98.9%; Pred. No. 8.
                                                                                                              beta
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Last annotation updat
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                                                                                                           subdivision;
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                 Brodeur B.R.;
                                                                                                                                                                                                                                      174
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                                                                                                         Neisseriaceae;
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Best Local :
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTER MEMBRANE PROTEIN PRECURSOR.
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P95371
P95371;
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                        Signal.
                                                                                                                                                                                                                                                                                                                                                                                           directed against Neisseria meningitidis NspA outer membrane Infect. Immun. 67:4955-4959(1999).
EMBL; U52067; AAB41579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Mai Bactericidal and cross-protective activities of a monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99386904; PubMed=10456958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=MCH 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=487;
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01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moe G.R., Tan S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=NGP165,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Differences in Surface Expression among Neisseria meningitidis Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                          61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
         61
                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                               1 MKKALATLIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
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; U52066; AAC35000.1; -.

; AF175683; AAD53286.1; -.

; AF175680; AAD53283.1; -.

; AF175682; AAD53285.1; -.

erPro; IPR003394; Opacity.
FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                       {\tt MKKALAALIALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
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                                                                                                                                                                                                                                                                                                                                           PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                   IPR003394; Opacity.
                                                                                                                                                                                                                                                                                175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 03, Created)
(TrEMBLrel. 03, Last sequence up
(TrEMBLrel. 19, Last annotation
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                           19 P
18572 MW;
                                                                                                                                                                                                         96.6%;
97.1%;
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98.3%;
                                                                                                                                                                                      0;
                                                                                                                                                                                    Score 838.5; DB:
Pred. No. 3.4e-62;
0; Mismatches '
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                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 854; DB 2;
Pred. No. 1,7e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                         DlEA8F2FF5CC2FEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E8B02767DDC6FE19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamel J., Brodeur B.R., Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Neisserial B strains.";
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                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                            Length 175;
                                                                                                                                                                                 Indels
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Best Local :
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Q51124;
Q1-NOV-1996
Q1-MAY-1997
Q1-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P95343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OUTER MEMBRANE PROTEIN PRECURSOR.
Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                           OPA.
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                       Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
Heckels J.E., Cannon J.G., Achtman M.;
"Recombinational reassortment among opa genes from ET-37 complex
Neisseria meningitidis isolates of diverse geographical origins.";
Microbiology 14:157-166(1998).
EMBL; U37255; AAC46101.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                        MEDLINE=98129089; PubMed=9467908;
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     Pfam;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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EMBL, AE006143; AAK03109.1; ...
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                                                                                                                                               RASVDLGGSDSF----SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGE 165
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RESULT 12
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Best Local
          Achtman M.;
"Clonal descent and microevolution of Neisseria meningitidis during 30 years of epidemic spread.";
                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                          MEDLINE-98010345; PubMed-9350862;
Morelli G., Malorny B., Mueller K.,
                                                                                                                                               Bacteria;
                                                                                                                                                                                   OPACITY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S. Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; "Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis.";
                                                                                           STRAIN-Z3906;
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=487;
                                                                                                                                                          Neisseria meningitidis
                                                                                                                                                                                                                                            Q9R719
                                                                                                                                                                                                                                                        Q9R7I9
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EMBL, AJZ92238; CAC36361.1; -.
Interpo; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLEL. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                    184 YHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGVRYRF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21221108; PubMed-11287631;
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                                                                                                                                                                                                                                                                                                                                                                         124 AVYDFNTGSREKPYAGVRVAYGHVRHSIDSTKKTTNVLTVPTNIPGGTPTIYNQGSTQDA
                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                              64 DFGDWRIAADYASYRKWNDNKYSVNTKNVQVNKSNGNRQDLKTENQENGTFHAVSSLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 RINDLREAVDYTRYKNY-------KAPSTDFKLYSIGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AALAEGA-SGFYVQADAAHA------KASSSLGS-----AKGFSPRISAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AASEDGSRSPYYVQADLAYAAERITHDYPKASGANNTSTVSDYFRNIRAHSIHPRVSVGY 63
                                                                                                                                                                                                                                                                                                                                                                                               PF02462; Opacity; 1.
ER 1 1
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                                                                                                                                              Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AA; 26923 MW; 4923ACF9484BF183 CRC64;
                                                                                                                                                                                                                                                        PRELIMINARY;
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29.7%;
                                                                                                                                              beta
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                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            Created)
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Pred. No. 1.2e-12;
                                                                                                                                           subdivision;
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                                                          Seiler A.,
                                                                                                                                                                                                                                                   234 AA
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                                                                                                                                         Neisseriaceae;
                                                         Wang J., del Valle J.,
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                                                                                                                                           Neisseria
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                                                                                                                                  Query Match
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Best Local
                                                                                                                                                                             Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                   years of epidemic spread.";
Mol. Microbiol. 25:1047-1064(1997).
EMBL; AF001195; AAC32716.1; -.
                                                                                                                                                                                                                                                                                       MEDLINE=98010345; PubMed=9350862; Morelli G., Malorny B., Muller K.,
                                                                                                                                                                                                                                                                                                                                                                                                                      OPACITY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S. Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; "Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of subgroup III Neisseria Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; ANO1194; AAC32715.1; --
EMBL; ANO1194; AAC32715.1; --
EMBL; ANO3394; Opacity.
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                     InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
Bacteria; Proteobacteri
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                                                                                                                                                                                                                                                                  "Clonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 SSVGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGMRYHF 234
55 RINDLRFAVDYTRYK----NYKAPSTDFK--
                                                                  16 AALAEGA-SGFYVQADAAH------AKASSSLGS-----AKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
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                                     4 AASEDGSRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHSIHPRVSVGY 63
                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 DFGDWRIAADYASYRKWKESNYSKKYTEFKHQNGNKQEDKTEHQGNGSFHATSSLGLSAI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AASEDGSRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHSIHPRVSVGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDFKLNDKFKPYIGVRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSI
                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                    Similarity
                                                                                                                                                                                                                                                         _descent_and microevolution of Neisseria meningitidis during 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                         Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                            234 AA; 26134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA; 26161 MW;
                                                                                                     Conservative
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                                                                                                                 28.0%;
29.3%;
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                                                                                                  30;
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                                                                                                                Score 243;
Pred. No.
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                                                                                                                                                         005AD356E93BCC50 CRC64;
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                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                     Seiler A., Wang
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                                                                                                                1.3e-12;
                                                                                                                              DB 2;
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                                                                                                                            Length 234;
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             LYSIGASAI
                                                                                                                                                                                                                                                                                  del Valle J.,
                                                                                                 74;
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RESULT 14
Q9R718
ID 908717
AC Q9R71
DT 01-M
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Q9K4T9
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Best Local
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01-MAY-2000
01-DEC-2001
                                                                                                                                                         Q9K4T9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9R7I8
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Mol. Microbiol. 25:1047-1064(1997).
EMBL; AF001196; AAC32717.1; -.
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                                                                                                                                                                                                                                                                                                       Q9K4T9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morelli G., Malorny B., Muller K.,
SEQUENCE FROM N.A
                                                                              Neisseria lactamica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Clonal descent and microevolution of Neisseria meningitidis during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98010345; PubMed=9350862;
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                                                    NCBI_TaxID=486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AASEDGSRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRTHSIHPRVSVGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGMRYHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDFKLSDKFKPYIGVRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDFKLNDKFKPYIGYRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGDWRIAADYASYRKWKESNYSKKYTEFKHQNGNKQEDKTEHQGNGSFHATSSLGLSAI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RINDLRFAVDYTRYK-----NYKAPSTDFK-----
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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29.3%;
                                                                                 beta subdivision; Neisseriaceae; Neisseria.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                      Toleman M.A., Aho E., Virji M.;
"Antigenic relatedness of commensal and pathogenic neisserial adhesins genetic and functional analyses of commensal Opa proteins.";
Submitted (APR-200) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ28888; CAB93949.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                           SIGNAL
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completed: October 28, ne : 20.9713 secs
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                                             ASAIYDFDTQSPVKPYLGARLSLNR------ASVDLGG------SDSFS 121
                                                                                             ISAIYDFDTGTRFKPYVGARVGLGKIRHSIALEDKAEIIIGNIPSGGLKDAHPPIHESHS 182
                                                                                                                                          SYGYDFGNWRIALDYARYNKWKHGKHIRTEQNKSYQNGTSYKLIADHTDKGTFKAESNYG
                                                                                                                                                                  SAGYRINDLRFAVDYTRYKNYK------
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26094 MW; 3
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             2002, 16:02:39
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                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                          65; Indels
                                                                                                                                                                                                                                                                Length 232;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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1. /SIDSI/gcgdata/g
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870
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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96	96	101	106	125	133	747	813.5	825	84	870		SCOTE		
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21	21	16	22	16	17	22	17	17	17	17		7		
AAY97900	AAY96098	AAR66294	AAB47447	AAR73911	AAW04912	AAB19895	AAW04892	AAW04891	AAW04893	AAW04894		3		SUMMARIES
Actinobacillus ple	Actinobacillus ple	Non-typable Haemon	MOMP PS. Haemonhi	Neisseria meningit	N. meningitidis 60	Neisseria meningit	Proteinase K resis	Proteinase K resis	Proteinase K resis	Proteinase K resis	Description			

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9.2	•	•	•	•	•	•		•		٠	9.3	9.4	9.4	•	٠	9.5	9.5	9.6	9.6	9.9	9.9		•	10.1	٠	•			10.9		•	11.0
273	270	270	270	270	266	260	259	15	350	350	279	708	708	162	889	624	610	534	339	568	215	215	16	573	500	364	364	364	797	369	257	212
18	22	21	19	19	20	20	21	17	22	9	17	21	19	17	19	19	19	21	21	17	21	21	17	19	22	21	21	21	20	21	22	22
AAW24665 AAW24665	AAE13029	AAY71921	AAY10954	AAY11014	AAY34407	AAY34541	AAG45506	AAW04909	AAB59179	AAP82053	AAW02369	AAY78360	AAW73022	AAR96207	AAW68208	AAW68204	AAW68206	AAG09860	AAG52873	AAR96210	AAY97897	AAY96096	AAW04901	AAW68202	AAB65766	AAY97899	AAY96097	AAB44588	AAY36955	AAB44589	AAU38252	AAU34556
H. pylori outer me H. pylori outer me		licobacter r	pylori ORF			Porphorymonas ging	-	N. meningitidis 60	Protein associated	Outer membrane pro	Proteinase K varia	H. pylori bacteria	Helicobacter pylor				liss		Arabidopsis thalia	_	Actinobacillus ple	tinobacillus n	meningitidi	M. catarrhalis str			illus			gene	almone	coli cellular

ALIGNMENTS

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RESULT 1
AAW04894
        Brodeur BR,
                        (IAFB-) IAF BIO VAC INC.
                                           04-AUG-1995;
17-MAR-1995;
                                                                                                                                                              Key
                                                                      15-MAR-1996;
                                                                                        26-SEP-1996.
                                                                                                         WO9629412-A1
                                                                                                                                    Protein
                                                                                                                                                    Peptide
                                                                                                                                                                              Neisseria meningitidis strain b2.
                                                                                                                                                                                            Proteinase K reistant; Neisseria meningitidis;
Neisseria gonorrhoeae; antibody; detection; probe; surface protein;.
                                                                                                                                                                                                                       Proteinase K resistant N. meningitidis 22 kD surface protein.
                                                                                                                                                                                                                                            22-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                AAW04894 standard; Protein; 174 AA.
      Hamel J, Martin D,
                                          95US-0001983.
95US-0406362.
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                                                                                                                                  /label= sig_peptide
20..174
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      Rioux C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 10; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strains - useful for prodn. of antibodies or diagnosis of, N. meningitidis infection
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                                                                                                                                                                                                                                         Key
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                                                               04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                    Neisseria
                                                                                                                                                                                                                                                                                                           Proteinase K reistant; Neisseria meningitidis;
                                                                                                                                                                                                                                                                                                                                   Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                                         AAW04893;
            Brodeur
                                                                                                        15-MAR-1996;
                                                                                                                                                            W09629412-A1
                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                               Neisseria
                                                                                                                                                                                                                                                                                                                                                               22-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW04893 standard;
                                                                                                                                 26-SEP-1996
                                    (IAFB-) IAF BIO VAC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
            BR,
                                                                                                                                                                                                                                                                                               gonorrhoeae;
                                                                                                                                                                                                                                                                    meningitidis strain Z4063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 AA;
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                                                                                                                                                                                                                                                                                                                                                               (first entry)
            Hamel J,
                                                               95US-0001983
95US-0406362
                                                                                                        96WO-CA00157
                                                                                                                                                                                                  /label= sig_peptide
20..174
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                      /label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 870; DB 17; 100.0%; Pred. No. 3.8e-85;
                                                                                                                                                                                                                                                                                               antibody; detection; probe;
            Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                   174
            Ď,
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            Rioux C;
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                                                                                                                                                                                                                                                                                                surface protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A proteinase K resistant surface protein has been isolated from 4 strains of N. meningliddis (AART3903) to AART39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningliddis on by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningliddis infection. The antigen may also be used to detect antibodies specific to N. meninglitidis
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N-PSDB; AAT39041.
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                                                             04-AUG-1995;
17-MAR-1995;
                                                                                                                           26-SEP-1996.
                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                  Proteinase K reistant; Neisseria meningitidis;
Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                        Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                           AAW04891;
                                                                                                                                                                                                                                                                                                                                                                                                     AAW04891 standard; Protein;
          Brodeur BR,
                                   (IAFB-) IAF BIO VAC INC.
                                                                                                    15-MAR-1996;
                                                                                                                                                       W09629412-A1
                                                                                                                                                                                           Protein
                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                           Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166;
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                                                                                                                                                                                                                                                           meningitidis strain 608B
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
          Hamel J,
                                                           95US-0001983
95US-0406362
                                                                                                    96WO-CA00157
                                                                                                                                                                                          /label= sig_peptide 20..174
                                                                                                                                                                                                                                 Location/Qualifiers
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95.48;
            Martin
                                                                                                                                                                                mat_protein
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Pred. No. 2.7e-81;
          D
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            Rioux C;
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WPI; 1996-443187/44.

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 1; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                   Brodeur BR,
                                                                                            04-AUG-1995;
17-MAR-1995;
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                                                                                                                                                                                                                                                                               Protein
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                                                   (IAFB-) IAF
                                                                                                                                                  15-MAR-1996;
                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
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                   Hamel J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding the antigen, or their fragments, can be used the detection of pathogenic Neisseria bacteria.
                                                                                          95US-0001983
95US-0406362
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20..175
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94.3%;
                   Martin
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antibody; detection; pr
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Pred. No. 2.5e-80;
                   D,
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                   Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 kD surface
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RESULT 5
AAB19895
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Best Local :
                                                                                                                                                                     Region
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strains - useful for prodn. of antibodies for immunisation against,
or diagnosis of, N. meningitidis infection
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Region
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                                                                    Region
                                                                                                    Region
                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                              Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNY IGKVNTVKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKKALAALIALAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                              infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                              meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                  /note= ";
105..114
                                                                                                    /note=
78..88
                                                                                                                                      /note=
63..74
                                                                                                                                                                        /note=
51..62
                                                                                                                                                                                                                                       /note=
27..37
                                                                                                                                                                                                                                                                         /note-
18..26
                                                                                                                                                                                                           40..50
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                      /note=
                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.5%;
              "transmembrane
                                                "surface-exposed connecting
                                                                                    "transmembrane beta-strand"
                                                                                                                    "transmembrane
                                                                                                                                                      "surface-exposed
                                                                                                                                                                                       "transmembrane beta-strand"
                                                                                                                                                                                                                       "transmembrane beta-strand"
                                                                                                                                                                                                                                                         "surface-exposed
                                                                                                                                                                                                                                                                                          "transmembrane beta-strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                            therapy; vaccine; meningococcal B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 813.5;
Pred. No. 4.3e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 813.5; DB 1
No. 4.3e-79;
                                                                                                                  beta-strand
                                                                                                                                                     connecting
                                                                                                                                                                                                                                                       connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitidis
                                                loop"
                                                                                                                                                      loop"
                                                                                                                                                                                                                                                       loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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RESULT 6
AAW04912
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                                                                                                                                                                                                                                                                                                                       BXXXX
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                                                                                                                                         Q
                                                                                                                                                                   밁
                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                       (iii) mixtures of 1 or more Neisserial protein and 1 or more Neisserial nucleic acid. The proteins and nucleic acids are preferably from different Neisseria spp., especially Neisseria meningitidis and Neisseria gonorrhoeae, but may be from the same species. A claimed composition includes the NapA protein, preferably in mature form. The compositions are used e.g. as immunogenic compositions, vaccines or diagnostic reagents. They are used to treat or prevent Neisserial infection, to detect the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria, and/or as reagents which can raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of the Neisseria meningitidis NspA protein, which contains 8 transmembrane beta-strands and 4 surface-exposed connected loops. Recombinant NspA is being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition comprising first and second biological molecules from a Neisseria bacterium, useful as vaccines or immunogenic compositions for treating Neisserial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1999; 99GB-0011692.
19-AUG-1999; 99GB-0019705.
09-MAR-2000; 2000GB-0005730.
   22-DEC-1996
                           AAW04912;
                                                  AAW04912 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      combination compositions comprising: (i) 2 or more Neisserial proteins, (ii) 2 or more different Neisserial nucleic acids; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                               against Neisserial bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease caused by all serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developed as a vaccine for the prevention of meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; Fig 32; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000; 2000WO-IB00828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200071725-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                   121
                                                                                                                                                                     61
                                                                                                                                                                                             80
                                                                                                                                                                                                                                  20 EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 79
                                                                                                                             NVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                 LYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSFSKTSAGLGVLAGVSYAVTP 139
                                                                                                                                                                                                                     EGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 60
                                                                                                                 NVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
                                                                                                                                                                   LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-025167/03
                                                                                                                                                                                                                                                                       146;
                                                                                                                                                                                                                                                                                                                       155 AA;
                                                                                                                                                                                                                                                                       Conservative
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "transmembrane beta-strand"
131..145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                  85.9%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "surface-exposed connecting loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "transmembrane beta-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rappuoli R;
                                                   25
                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                 Score 747; DB 22;
Pred. No. 4.8e-72;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides
                                                                                                                  155
                                                                                                                                                                                                                                                                                              Length 155;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                     0;
 멁
                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Sharma LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N. meningitidis 608B peptide CS-857.
                                                                                                                 06-APR-1995.
                                                                                                                                          WO9509232-A.
                                                                                                                                                                                                     Neisseria meningitidis; opacity related protein POPM3; vaccine; meningitis related homologous antigenic sequence; MRHAS; RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
                                                                                                                                                                                                                                                      Neisseria meningitidis opacity related protein POPM3
                                                                                                                                                                                                                                                                                  05-DEC-1995
                                                                                                                                                                                                                                                                                                          AAR73911;
                                                                                                                                                                                                                                                                                                                                  AAR73911 standard; protein; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 24; Page 84; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brodeur BR, Hamel J, Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-AUG-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteinase K reistant;
Neisseria gonorrhoeae;
                       (SHAR/) SHARMA L R. (VALS/) VAN ALSTYNE D.
                                                                                       28-SEP-1994;
                                                                                                                                                                  Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09629412-A1
                                                              28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 AA;
 Van Alstyne D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                               (first entry)
                                                              93US-0127499
                                                                                       94WO-CA00516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0001983.
95US-0406362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-CA00157
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
or diagnosis of, N. meningitidis infection
                                                                                                                                                                    Example 9 describes the epitope mapping of the 22 kD N. meningitidis protein. Identification was accomplished using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis; epitope; mapping; antibody; detection; probe; surface protein.
                           Score 133; DB 17;
Pred. No. 2.3e-07;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rioux C;
   0
                                                       Length
0;
Gaps
0
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ARBSULT 8
AAB47A47
ID AAB4
XX AAB4
XX AAB4
XX SUIF
KW SUIF
KW IOON
KW IOW
XX IO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SXCCCCCCCCXXXIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR73911 is the Neisseria meningitidis opacity related protein POPM3. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73889 and AAR73901, which are recognised by a monoclonal antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis treatments. The peptides may also be used as vaccines against meningitis.

NB: Identified by matching corresponding MRHAS peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB47447 standard; Protein; 353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 47; Fig 5/10; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) and corresp. antibodies for the treatment of meningitis - the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used
                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            otitis media; sinusitis; conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surface exposed loop; major outer membrane protein P5; MOMP P5;
non-typeable H. influenzae; ntH1; LB1(f) peptide; B cell epitop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB47447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
    23-AUG-2001
                                                   WO200161013-A1
                                                                                                                                               Domain
                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting and preventing meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-147431/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ASSLGLSAIYDFKLKGKFKPYIGARVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AALIALALPAAALAEGASGFYVQADAAH------AKASSSLGS------AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYSIGASVIYDFDTQSPVKPYFGARLS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLLFSSAAQAASEDRRSPYYVQADLAYAAERTTHDYPQATGANNTSTVSDYFRNIRAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                   /label= Loop 1
/note= "Extracellular domain"
89..100
                                                                                                                                          /note= "Extracellular 181..204
                                                                                            /label= Loop 4
/note= "Extracellular domain"
                                                                                                                                                                                        /label= Loop 3
                                                                                                                                                                                                                                       /note= "Extracellular domain"
                                                                                                                                                                                                                                                               /label= Loop 2
                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%; 25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125; DB 16; Pred. No. 2.2e-05;
                                                                                                                                                                   domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B cell epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KAPSTDFK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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    FT FT XXX XXX XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                    Ħ
                                                                                                                                                                                                                                                                                                                                                                          AAR66294
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the major outer membrane protein P5 of non-typeable H. influenzae. One or more surface exposed loops of this protein may be replaced with a modified peptide of the invention. Each of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP P5 from strain ntHill28, representing amino acids Argl17 to Gly135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recembinant outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                environment in the recombinant outer membrane protein. The mod
MOMP P5 may be used to induce an immune response in a mammal to
prevent or treat Haemophilus influenzae infection or associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g.,
Peptide
                                                                      Key
                                                                                                                                                                                                                                                                                                                                                    AAR66294 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               otitis media and conjunctivitis -
                                              Region
                                                                                                                                                              Fimbrin
                                                                                                                                                                                                         Non-typable Haemophilus influenza (NTHi) fimbrin protein.
                                                                                                                                                                                                                                                          09-AUG-1995
                                                                                                                                                                                                                                                                                                        AAR66294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2001; 2001WO-EP01556
                                                                                                               Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000; 2000GB-0003502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LTRVGKYRPQDKPNTALNYNPWIGSINAGISYRF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALAALIALALAALAEGA---SGFYVQADAAHAKASSSLGS-----AKGFS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVYGKAGVALVRSDYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLEYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGVFGGYQTLNQNNLGLAVELGYDDFGRAKGREKGKTVVKHTNHGTHLSLKGSYEVLEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPYFGARLSLNRASAHLGGSDSFSKTSAG-----LGVLA-GVSYAVTPNVDLDAGY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRISAGYRI----NDLRFAV-----DYTRYKNYKAPSTDFKLYSIGA--SVIYDFDTQSPV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQASFHDGLRALAREYKVGYHRNSFT 60
                                                                                                                                                           protein; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RYNYVGKVNTVKNVRS--GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AA;
                                                                                                             influenza strain 1128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Denoel P,
                                                                                                                                                                                                                                                        (first entry)
/label= amino terminus 234..249
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%; 25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poolman J, Thonnard J;
                                                                                                                                                              otitis media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                    359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106; DB 22
Pred. No. 0.0063;
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                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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90;

40;

Gaps

9

Length 353; Indels

The modified

TD;

is to be inhibited,

OmpA2 of

in fusion

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AAY96098
ID AAY96
XX AAY96
XX TI9-DE
XX U19-DE
XX U19-DE
XX U19-DE
XX Outer
KW Outer
KW dual
XX Actin
XX EP103
                                                                                                                                                                                                                                                                                                                                                                                              Ωy
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                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause otitis media. Finbrin protein is produced by culturing a transformed microbial host, pref. E.coli, Sporodoptera frugiperda or a mucosal pathogen. Finbrin protein (FP) produced by this process is claimed. The FP protein migrates in polyacrylamide genes to a posn. equiv. to a mol. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The fimbrin proteins from 15 randomly selected type b and non-typable clinical isolates of Haemophilus influenzae share common epitopes. Thus frimbrin isolated from non-typable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
                                   Actinobacillus
                                                                                                                 Actinobacillus
                                                                                                                                                   19-DEC-2000
                                                                                                                                                                                    AAY96098;
                                                                                                                                                                                                                 AAY96098 standard; Protein; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (-OIHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9426304-A
                                                                                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                 114
                                                                                                                                                                                                                                                                                               174 VLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASVIY-DF---DTQSPVKP-----YFGAR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALAALIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG
                                                                                                                                                                                                                                                                                                                                                                                                LSLNRASAHLGGSDSFSKTSAGL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt MKKTATALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1995-006359/01.
                                                                                                                                                                                                                                                                                                                             VTPNVDLDAGY -----RYNYVGKVNTVKNVRS -- GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                               LSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYA
                                                                                                                                                                                                                                                                                                                                                                                                                              YRRNTFTYGV----FGGYQILNQD--NFGLAAELGYHDFGRAKLREAGKPKAKHTNHGAY 113
                                                                                 membrane protein; OmpA1; vaccine; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OIHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ78916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 AA;
                                                                response; immunogen; pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kolattukudy PE,
                                   pleuropneumoniae
                                                                                                                 pleuropneumoniae OmpA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0065442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US05477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sirakova
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
   ##XEXEXEXXX
                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins of the invention that are used as vaccines eliciting a condition of the invention that are used as vaccines eliciting a condition of the invention of the fusion proteins comprise: a first protein that is endogenous to a vertebrate, the activity of which is to be inhibited within the vertebrate, and which is incapable by itself of eliciting an effective immuncinhibitory response in the vertebrate; and a second protein, which is an immunogen from a pathogen capable of infecting the vertebrate, and which causes the vertebrate's immune system to recognise the first protein, producing a response that inhibits the activity of the first protein, and also protecting the vertebrate from infection by the pathogen when the vertebrate is vaccinated with the fusion protein in the present case, a fusion protein of cholecystokinin and OmpA2 is useful for encouraging appetite in swine while simultaneously providing a protective immune response against porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                             Actinobacillus pleuropneumoniae outer membrane protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fusion protein for producing a dual immune response comprise peptide analogous to an endogenous peptide which is to be inhibit connected to a peptide analogous to an immunogen from a pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2000;
                OmpA2; outer membrane
                                                                                 11-SEP-2000
                                                                                                                                                AAY97900 standard; Protein; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2000.
                                                                                                                                                                                                                                174
                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKALAALIALALPAAALAEGA---SGFYVQADAAHAKASSSLGSAK-GFSPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ocal
   scrofa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is that of outer membrane protein (
                                                                                                                                                                                                                                                              VTPNVDLDAGYRYNYVGKVNTVKN--VRSG----
                                                                                                                                                                                                                                                                                           PSYEVLPDLDVYGKV----GVAVVRNDYKSY-GAENTNEPTEKFHKLKASTILGAGVEYA
                                                                                                                                                                                                                                                                                                                            ---SVIYDFDTQSPVKPYFGARLSLNRASAHLGG-----SDSFSKTSAGLGVLAGVSYA 136
                                                                                                                                                                                                                                                                                                                                                                                                                            MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                                                                                                                                                                                                                            ILP--ELAARVEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRF
                                                                                                                                                                                                                                                                                                                                                              YGINRNSVTYGVFGGYQILNQNNFGLATELGYDYYGRVRGNDGEFRAMKHSAHGLNFALK 118
                                                                                                                                                                                                                                                                                                                                                                                          -----ISAGYRI---NDLRFAVD--YTRYKNYKAPSTDFKLYSIGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 58-60; 93pp; English
serotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000EP-0301103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0120454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%;
23.6%;
protein;
antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Durtschi BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96;
Pred. No.
 APP; pneu
vaccine;
                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
             pneumonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yule
 cross-reactive
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Length 369

Indels

68;

Gaps

13;

49

85

pathogen;

OmpA2. swine;

-ELSAGVRVKF 174

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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   CC protein, OmpA2, from Actinobacillus pleuropneumoniae (APP) strain C P2420 (ARCC 98930). The invention relates to the novel APP outer CC membrane proteins Omp20, OmpW, OmpA2, OmpA1 and OmpA2 (ARY97896-Y97900) CC and to nucleic acids encoding them (AAA38554-A38585). APP is a Gram CC negative cocobacillus which is one of the most important swine CC pneumonic pathogens. 12 different serotypes of APP have been recognised CC which vary in geographic distribution. Prior art attempts at vaccinating CC against APP have produced mainly serotype-specific immune responses. In CC contrast, natural immunity to any one serotype seems to confer CC significant protection from disease caused by other serotypes, suggesting CC that natural exposure induces cross-reactive immunity to shared antigens. CC The novel outer membrane proteins of the invention are present in all 12 cc. Serotypes, and may provide a target for cross-protective immunisation. CC The novel outer membrane proteins and nucleic acids encoding them can be companied for the attractive apainst APP in swine. They can also be used as
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a low molecular weight outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 5; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA encoding them, for use as vaccines against the bacteria in swine - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ankenbauer RG, Baarsch MJ, (Warren-Stewart LM, Suiter BT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ankenbauer RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1001025-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                         174 ILP--ELAARVEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRF 224
                                                                                   137
                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-protection; diagnosis
                                                                                                                                                      86
                                                                                                                                                                                       59
                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                    1 MKKALAALIALALPAAALAEGA---SGFYVQADAAHAKASSSLGSAK-GFSPR-----
                                                                            VTPNVDLDAGYRYNYVGKVNTVKN--VRSG------ELSAGVRVKF 174
                                                                                                             PSYEVLPDLDVYGKV----GVAVVRNDYKSY-GAENTNEPTEKFHKLKASTILGAGVEYA
                                                                                                                                             ---SVIYDFDTQSPVKPYFGARLSLNRASAHLGG-----SDSFSKTSAGLGVLAGVSYA 136
                                                                                                                                                                                YGINRNSVTYGVFGGYQILNQNNFGLATELGYDYYGRVRGNDGEFRAMKHSAHGLNFALK 118
                                                                                                                                                                                                                                                   MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                                                                                                                                                                                                                  -----ISAGYRI---NDLRFAVD--YTRYKNYKAPSTDFKLYSIGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-320438/28.
DB; AAA38558.
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            for the diagnosis of APP infections.
                                                                                                                                                                                                                                                                                                                                                                                                 369 AA;
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pleuropneumoniae strain Pz420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0308262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Signal peptide"
20..369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                          11.0%; Score 96; L
23.6%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mature OmpA2"
                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos M,
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                          DB 21; Length 369; 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keich RL,
                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosey EL;
                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                  85
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                                                                        ş
                                                                                                                                                                                                     genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella Chevention is also useful for the identification of potential new targets of antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery for homologous nucleic acids which are required for cell proliferation in casential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part contains the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU34556
                                                                                                        Matches
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 10149; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli cellular proliferation protein #137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU34556 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002
55 RINDLRFAVDYTRYKNYKA------PSTDFKLYSIGASVIYDF-----
                                 1 MKKLTVAALAVTTLLSGSAFAHEAGEFFMRAGSATVRPTEGAGGTLGSLGGFSV-----
                                                              1 MKKALAALIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-611495/70.
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS52415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-269308P
                                                                                                11.0%; Score 95.5; DB 23.8%; Pred. No. 0.042; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall D,
                                                                                                                                DB 22;
                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick JD,
                                                                                                   Indels
                                                                                                                                Length 212;
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                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU38252
                                                                             The invention relates to antisense inhibitors of genes essential to component of the control of the control of genes essential to component of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU38252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU38252 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001;
                   ftp.wipo.int/pub/published_pct_sequences
                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Seq ID No 13845; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotics, comprise sequences of antisense nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 -- VDLDAGYRYNYVGKVNTVKNVRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLVNMSVWYM-----DIDTTANYKLG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DTQSPVKPYFGARLS-----LNRASAHLGGSDSFSKTSAGLGVLAGVSYAVTPN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFGDASSKFRPYVGAGINYTTFFDNGFNDHGKEAGLSDLSLKDSWGAAGQVGVDYLINRD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TNNTQLGLTFT----YMATDNIGVELLAATPFR-HKIGTRATGDIATVHHLPPTLMAQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prokaryotic cellular proliferation protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              typhi cellular proliferation protein #143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development ucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick JD,
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 AAB44589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                 The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be
                                                                                                                                                                                                 Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virulence gene protein #69
                                                                                                                                                                                                                                                                                                                                               09-APR-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200061724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB44589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB44589 standard; Protein;
Sequence
                                                   mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating
                                                                                                                                                       Claim 39; Pages 308-309; 322pp; English
                                                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN INC
                              wound infections.
                                           bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKALAALIALA--LPAAALAEGASGFYVQADAAHAK----ASSSLGSAKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLIGASVWYMDIDTTANYK-MGGVQQHDSVRLDPWVFMFSAGXR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VDLDAGYRYNYVGKVNTVKNVRSGE----LSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFGDSSSKVRPYVGVGVNYTTFFDNDFNDNGKKTGLSDLSFKDSXGAAGQVGVDYLINRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DTQSPVKPYFGARLS-----LNRASAHLGGSDSFSKTSAGLGVLAGVSYAVTPN
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DB; AAC79664.
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 369
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Pred. No. 0.062;
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                                           bronchopneumonias,
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Query Match Best Local Similarity

10.9%; 24.2%;

Score 95; Pred. No.

DB 0.1;

Length 369;

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RESULT 15
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 Query Match 10.9%; Score 94.5; DB 20; Best Local Similarity 29.6%; Pred. No. 0.32; Matches 34; Conservative 16; Mismatches 48;
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                                                                                        AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                       Sequence
                                                                                                                                                                                                                                                                                                Disclosure; Page 802; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                 Genome sequence of Chlamydia trachomatis
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                                                                                                                                                                                                                                                                                                                                                                                                       Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihapatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 SYAVTPNVDLDAGYRYNYVGKVNTVKN--VRSG-----ELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 PSYEVLPDLDVYGKVGIAVVRNDYKKY-GAE-NTNESTT-----KFHKLKASTILGAGV 170
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Search completed: October 28, Job time: 25.7145 secs
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                                                                                                                         74 PSTDFK----LYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSFSKTSA 125
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                                                                                                                                                                                                                  VQADAAHAKASSSLGSAKGFSPRISAGYRIND-LRFAVDY-----TRYKNYKA 73
                                                                                   PDLDSNKGFVSAAGLNVLYD-SIDNPRKPTMGIRSFLNXELSGLGGTYQFTKLTA 635
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Title:
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Maximum DB
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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      231628 segs, 24425594 residues
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Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/backfiles1.pep:*
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US-08-913-362-8
US-08-913-362-6
US-08-913-362-30
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US-08-127-499A-20
US-08-127-499A-20
US-08-467-722A-2
US-08-467-722A-3
US-08-913-362-15
PCT-US95-13749-5
US-09-336-447A-11
US-09-336-447A-11
US-09-336-447A-11
US-09-336-447A-15
US-08-913-362-23
US-08-913-362-14
US-08-913-362-14
US-08-913-362-13
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                         Sequence 8, Appli
Sequence 2, Appli
Sequence 30, Appl
Sequence 26, Appli
Sequence 20, Appli
Sequence 20, Appli
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Sequence 2, Appli
Sequence 15, Appli
Sequence 16, Appli
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Sequence 11, Appli
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Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	FACELL NO. 32120/4	Datast We Enjoy	7	Sequence 7. Appli	19	Sequence 4, Appli	Sequence 2, Appli	Sequence 4, Appli	sequence 2, Appli	rddu (cr. pomens	<u>,</u>	4	Sequence 3, Appli			Sequence 10, Appl

ALIGNMENTS

US-08-913-362-8

Sequence

Sequence 8, Application US/08913362 Patent No. 6287574 GENERAL INFORMATION:

APPLICANT: Brodeur, Bernar APPLICANT: Martin, Denis APPLICANT: Hamel, Josee APPLICANT: Rioux, Clement

Brodeur, Bernard Martin, Denis

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US-08-913-362-8
    Query Match
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTONNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                    TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            TELEPHONE: (202)672-5399
TELEX: 90417E
                                                        TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$\,08/913,362 FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                  TYPE:
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CITY: Washington
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Length 174;
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Best Local Similarity

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Pred. No. 3e-95;

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                                                               Matches
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                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    NAME: Bent, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 01 FILING DATE: 17-MAR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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STREET: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 6 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                         TELEX: 90413
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                                                                                                                                                                                        LENGTH:
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              1 MKKALAALIALALPAAALAEGASGTYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                         amino acid
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3000 K Street, N.W., Suite 500
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                                                                                                                                                                                        174 amino acids
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                                                                                                                                                                                                                                                        : (202)672-5300
(202)672-5399
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Martin, Denis
                                                               Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                          protein
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                                                                              95.9%;
95.4%;
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                                                                                                                                                                                                                                                                                                                                                                                 us 60/001,983
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                                                                              Score 834; DB 4; Length 174; Pred. No. 5.5e-91;
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Patent No. 6287574
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                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 1
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               121 SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                   61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                   1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                  FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                 amino acid
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Rioux, Clement
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                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                  Score 825; DB 4; Length 174; Pred. No. 6.4e-90; 2; Mismatches 8; Indels
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GENERAL INFORMATION:

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RESULT 5
US-08-913-362-4
: Sequence 4, Application US/08913362
; Patent No. 6287574
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US-08-913-362-30
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
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APPLICANT:
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                                                                                                         121 FSQTSXGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                               120 FSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                 61 FAVDYTRYKNYKXAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 120
                                                                                                                                                                                                     61 FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
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CITY: Washington
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                                                                                                                                                                                                                                                                                     1 MKKALAALIALALPAAALAEGASGTYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Hamel, Josee
Rioux, Clement
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3000 K Street, N.W., Suite 500
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                                                                                                      Sequence 26, Application US/08913362 Patent No. 6287574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                    APPLICANT: Brodeur,
APPLICANT: Martin, I
APPLICANT: Hamel, JG
APPLICANT: Rioux, Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
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FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0: FILING DATE: 17-MAR-1995 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
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                                                                                                                                                                                                                        121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                            120 FSKTSAGLGVLAGVSYAVTPNVDLDAGYRVNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                             61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                                                                                                                                                                                                                                                  61 FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDS 119
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 93.5%;
Local Similarity 93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/913,362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 amino acids
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3000 K Street, N.W., Suite 500
                                Martin, Denis
Hamel, Josee
Rioux, Clement
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SYSTEM: PC-DOS/MS-DOS
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PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
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Pred. No. 1.5e-88;
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US-08-127-499A-20
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                                                                                                                                                                                                                                                                                                      Patent No. 5510264
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, LAWTENCE RAJENDIA
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                STREET: 3000 K St
CITY: Washington
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                                                                                                                  COUNTRY:
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                                                                                                  RY: USA
20007-5109
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APPLICATION DATA:
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                                                                                                                                    D.C.
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                                                                                                                                                                  3000 K Street, N.W., Suite 500
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(202)672-5399
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                              APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-UN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARWA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREFO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDLUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (202)672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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5, 5556757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suite 500
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                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                     TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ASSLGLSATYDFKLKGKFKPYTGARVA 161
54 YRINDLRFAYDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPV----KP----YFGAR 104
                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 FSPRISAGYRINDLRFAVDYTRYKNY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 25.28; es 37; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/457,997B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 44114-2688
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                                                                       1 MKKALAALIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AALIALALPAAALAEGASGFYVQADAAH-----AKASSSLGS-----AKG 45
                                 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohio
                                                                                                                                                                                                                                                  359 amino acids

₹: Calfee, Halter and Griswold

Suite 1800 800 Superior Avenue

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                                                                                                           Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        12.0%; Score 104; DB 1; Length 359; 24.7%; Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                               34,829
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                                                                                                         29; Mismatches
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Pred. No. 4.8e-07;
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                                                                                                           Indels 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
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NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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174 VLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
                                  137 VTPNVDLDAGY-----RYNYVGKVNTVKNVRS--GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 VLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                   60
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                                                                                                                                                                                                                       1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
                                                                                                                                                                                                                                                        1 MKKALAALIALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG
                                                                       LSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYA
                                                                                                                                             YRRNTFTYGV----FGGYQILNQD--NFGLAAELGYDDFGRAKLREAGKPKAKHTNHGAY 113
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                                                                                                                                                                                                                                                                                                                   Similarity
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|VENTION: Otitis Media Vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                            -----GVLA-GVSYA 136
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RESULT 11

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RESULT 12
US-08-913-362-15
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Best Local Similarity
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APPLICANT:
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APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT FILLING DATE: 199-06-21
CURRENT FILLING DATE: 199-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 573
                                    PRIOR APPLICATION DATA:
                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hamel, Josee APPLICANT: Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 SAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 --DTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSVGKFN---ATAALGGYGSKSAV 535
                                                                                                         APPLICATION NUMBER: US/O
FILING DATE: 13-NOV-1997
                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                             STREET: 3000 K St
CITY: Washington
                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                            COUNTRY:
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COPE, LESLIE D.
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                                                                                                                                                                                                                                                                                                                                E: Foley & Lardner 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin, Denis
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25.1%;
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Pred. No. 0
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Best Local Similarity
""+"hes 16; Conserva
                                                                                                                                               δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown ; MOLECULE TYPE: protein PCT-US95-13749-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
PCT-US95-13749-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-913-362-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application PC/TUS9513749 GENERAL INFORMATION:
                                                                                                                                                                                     Matches
                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
MOLECULE TYPE: p
ORIGINAL SOURCE:
ORGANISM: Neis
STRAIN: 608B
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Amgen Inc.
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
106 SLNRASAHLGGSDSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGE 165
                                    451 DDNWGVIGSFA--YTHQGYDFFYGSNKFGHGDVDYYSVTMGPSFRINEYVSLYGLLGAAH 508
                                                                                                            396 SVPGRGSIEGRASVNVY---AASESSISIGYAQSHVKENGYTLDNDPKGFN--LKYRYEL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 91320-1789
                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1840 Dehavi.
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
047998/0128
                                                                                                                                               12 ALPAAALAEGASGFYVQADAAHAKASSSLGSA------KGFSPRISAGYRI 56
                                                                                                                                                                                 Match 9.9%; Score 86; DB 5 Local Similarity 26.9%; Pred. No. 0.12; Local Similarity 25; Mismatches
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FAVDYTRYKNYKAPST 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FAVDYTRYKNYKAPST 16
                                                                      NDL-----RFAVDYTR-----YKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                 568 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.0%; Score 87; DB 4; L
100.0%; Pred. No. 0.00043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                     DB 5; Length 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                   Indels
                                                                                                                                                                                   40;
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US-09-336-447A-11
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09336447A Patent No. 6310190
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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    Best Local Similarity
                                                                                                                                                                                APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: ANCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09336447A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                            APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                             LENGTH: 624
TYPE: PRT
                                                                                    ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 610
TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIGVNYEF 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 KTSAGLGVLAGVSYAYTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 SKYENGMAAQAALSGLEQPYSVGKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAFDGRITALD 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 GKYKASV-FDESISASKISMAYG--AGVQFNPLPNFVIDASYEYS---KLDSIK-VGTWM 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 LSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562 LGAGYR 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TRYKN----YKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSFS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AEGASGFYYQADA-----AHAKASSSIGS-AKGFSPRISA-GYRIN--DLRFAVDY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
    9.5%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.5%; Score 83; DB 4; Length 610; 26.0%; Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
Score 83; DB 4; Length 624; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NATAALGGYGSKS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
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                                                                                                                                                                                                                                                                    Matches
585 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIGVNYEF 624
                                                                                 547 SKVENGMAAQAALSGLFQPYSVGKF------NATAALGGYGSKS
                                      122 KTSAGLGVLAGVSYAVTÞNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                     487 ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAFDGRITALD 546
                                                                                                                                                                                                             19 AEGASGFYVQADA-----AHAKASSSLGS-AKGFSPRISA-GYRIN--DLRFAVDY 65
                                                                                                                          66 TRYKN----YKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSFS 121
                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                               21; Mismatches
                                                                                                                                                                                                                                                        55; Indels
                                                                                                                                                                                                                                                        52; Gaps
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Search completed: October 28, 2002, 16:04:21 Job time: 10.4864 secs

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Scoring table:
                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                          Perfect score:
                                                                                                                                           October 28, 2002, 15:58:04; Search time 12.4821 Seconds (without alignments) 1339.485 Million cell updates/sec
                               BLOSUM62
                                                              US-09-684-883-8
870
1 MKKALAALIALALPAAALAE.....VNTVKNYRSGELSAGVRVKF 174
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compus
                                                                                                                                                                                                                                                                                                Compugen Ltd
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Total number of hits satisfying chosen parameters:

283138

283138 seqs, 96089334 residues

Database PIR_71:* Maximum Match 100% Listing first 45 summaries pir3:* pir2:* pir1:*

score d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

4.	44	43	42	41	40	39	38	37	36	ω	34	ω ω	32	31	30
114	116.5	120	120.5	122.5	124.5	124.5	125	125	129	134	144.5	176.5	184.5	194.5	206
13.1	13.4	13.8	13.9	14.1	14.3	14.3	14.4	14.4	14.8	15.4	16.6	20.3	21.2	22.4	23.7
182	264	192	201	70	284	281	170	168	239	187	210	121	235	214	239
Ν	N	N	N	N	N	N	N	N	N	Ν	Ν	2	N	N	N
AI0353	I54668	S44712	S16286	F64066	G98271	AH3012	T10256	S08513	AH0541	S20044	S77737	164187	S44707	S44706	S28630
attachment invasio	heat resistant ago	opacity protein on		probable outer mem	hypothetical prote	outer surface prot	opacity protein-re	opacity protein-re	e outer m			opacity protein ho		-	opacity protein op

ALIGNMENTS

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491 A;Reference number: A81775; MUID:20222556 A;Accession: B81932

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-174 < PAR>

A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84143.1; PID:g737 A;Experimental source: serogroup A, strain Z2491

C; Genetics: nspa; NMA0862

QY Matches Query Match Local 1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60 166; h 95.9%; Score 834; DB 2; Length 174; Similarity 95.4%; Pred. No. 3.3e-67; Conservative 2; Mismatches 6; Indels 0; Gaps 0,

δÃ 61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120

1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60

B

밁 61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDEDTQSPYKPYLGARLSLNRASYDLGGSDSF

B Q

RESULT 2 G81174

Outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: G81174
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Ti, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Ilile: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; A;Accession: G81174 A;Status: preliminary

```
A;Molecule type: DNA
A;Residues: 1-174 <TET>
A;Cross-references: GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAF41081.1; PID:g722588
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S16610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S16610
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene:
C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opacity protein opaK precursor - Neisseria gonorrhoeae (strain MS11) (fragments) N;Alternate names: outer membrane protein opaK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δõ
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                                                                                                                                                                                                                                                                                                                                                                                           F;96-134/Domain: extracellular #status predicted <EXT2>
F;102-129/Region: hypervariable region HV1
F;103-149/Domain: transmembrane #status predicted <TM4>
F;155-165/Domain: transmembrane #status predicted <TM5>
F;166-212/Domain: extracellular #status predicted <EXT3>
F;166-212/Domain: hypervariable region HV2
F;117-218/Region: hypervariable region HV2
F;213-225/Domain: transmembrane #status predicted <TM6>
F;229-237/Domain: transmembrane #status predicted <TM6>
F;229-237/Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain MS11, variant 4.8
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    맑
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F;238-252/Domain:
F;253-261/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;51-61/Region: semivariable region
F;76-84/Domain: transmembrane #status predicted <TM2>
F;89-95/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;34-42/Domain: transmembrane #status predicted <TMl>F;43-75/Domain: extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: cell surface component; transmembrane proteir F;1-10,11-23/Domain: signal sequence (fragments) #status F;24-261/Product: opacity protein opak #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X52364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S16610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: opacity protein Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SKTSAGLGVLAGVSYAVTÞNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
    21
                                                                                15 AAALAEG-ASGFYVQADAAHAKA-----SSSLGSAKG-----FSPRI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMB0663
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AQAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKGTTISTVSDYFRNIRTHSIHPRV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-261 <BHA>
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                                                                                                                                                                                                 Score 237.5; DB 2;
Pred. No. 8e-14;
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Pred. No. 9.2e-67;
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predicted <TM8>
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                                                                                                                                                                                                                                           Length 261;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                    91;
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A; Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1
A; Note: the authors did not translate the sequence of the signal peptide
A; Note: expression of opacity proteins is regulated by the number of tran
of repeats place the start codon in frame with the rest of the protein
R; Taha, M.K.; So, M.; Selfert, H.S.; Billyard, E.; Marchal, C.
EMBO J. 7, 4367-4378, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S04380; S16504
R;Palmer, L.; Brooks, G.F.; Falkow, S.
Mol. Microbiol. 3, 663-671, 1989
A;Title: Expression of gonococcal protein
A;Reference number: S04380; MUID:89343653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fr C;Species: Neisseria gonorrhoeae
A;Variety: strain F62-SF
C;Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
E;1-10,11-23/Nomain: signal sequence (fragments) #status;
E;24-270/Product: opacity protein opaK #status predicted .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X13965
A;Experimental source: strain MS11A
A;Note: expression of opacity proteins is regulated by the number of translated repea of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Pilin expression in Neisseria gonorrhoeae is under both positive and negativ A;Reference number: S02017; MUID:89210824 A;Accession: S15504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S04380
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A; Residues: 1-270 < PAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;34-42/Domain: transmembrane #status predicted F;43-75/Domain: extracellular #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 259-270 <TAH>
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                                                                                                                                                                                                F;142-156/Domain: transmembrane #status predicted <TM4>
F;162-172/Jomain: transmembrane #status predicted <TM5-
F;173-221/Domain: extracellular #status predicted <EXT3>
F;178-227/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                        F;102-136/Region:
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                                                                                       F;262-270/Domain: transmembrane
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                                                                                                                  247-261/Domain:
                                                                                                                                             238-246/Domain:
                                                                                                                                                                                                                                                                                                                                                96-141/Domain: extracellular #status predicted <EXT2>
                                                                                                                                                                           222-234/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKNTQNAHRESDSIRRVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLSAVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKGNGNRTDLKAENQENGTFHAVSS
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                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status predicted <TM2>
transmembrane #status predicted <TM3>
                                                                                                                  transmembrane
extracellular
                                                                                                                                                                                                                                                                                                                     hypervariable region HV1
                                                                                                                                                                           transmembrane
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                                                                                                         #status predicted
#status predicted
#status predicted
                                                                                       #status
Score 236; DB 2;
Pred. No. 1.1e-13;
                                                                                       predicted
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                                 Length 270;
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Query Match Best Local Similarity

27.1%; 27.4%;

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A;Residues: 24-260 <KUP>
A;Residues: 24-260 <KUP>
A;Residues: 24-260 <KUP>
A;Cross-references: EMBL:Z18937; NID:g49333; PIDN:CAA79370.1; PID:g940799
A;Experimental source: strain MS11, variant F3
A;Experimental source: strain mS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated of rangard place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999 (;Accession: S16611; S36345; S28624 R;Bhat, K.S.; Gibbs, C.P.; Barra, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991 A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam: A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                 C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
E;1-10,11-23/Domain: signal sequence (fragments) #status protein
E;24-260/Product: opacity protein opaJ #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Note: the authors did not translate the sequence for the signal peptide A:Note: expression of opacity proteins is regulated by the number of translate the space the start codon in frame with the rest of the protein of repeats place the start codon in frame with the rest of the protein
                                              F;165-211/Domain:
F;170-217/Region:
                                                                                                                                                                                                                                                  F;34-42/Domain: transmembrane #status predicted <TM1>
F;43-74/Domain: extracellular #status predicted <EXT1>
F;51-60/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms A;Reference number: S36328; MUID:93178439
A;Accession: S36345
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments) N; Alternate names: outer membrane protein opa58 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
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                                                                                                        F;154-164/Domain:
                                                                                                                          F;134-148/Domain:
                                                                                                                                               F;101-128/Region:
                                                                                                                                                                    F;95-133/Domain: extracellular #status predicted <EXT2>
                                                                                                                                                                                                F;88-94/Domain: transmembrane #status
                                                                                                                                                                                                                             F;75-83/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: opaJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Kupsch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain MS11, variant 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X52371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-260 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S16611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.M.; Knepper, B.; Kuroki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHNWGRLENTR-FKTHEASLGVRYRF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEIVTTYPKEQNVAPSPIPGAPTKKPAHHESRSISSLGFGAVAGVGIDITPNLTLDAGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLNIQTQKTEHQENGTFHAASSLGLSTIYDFDTGSRFKPYIGARVAYGHVRHQVRSVEQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYFRNIRTHSVHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELGRNDNSASGVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKALAALIALALPAAALAEG---ASGFYVQADAAH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --NYKAPSTDFK-----LYSIGASVIYDFDTQSPVKPYFGARLSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GF-----SPRISAGYRINDLRFAVDYTRYK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                        transmembrane #status predicted
               hypervariable region HV1
transmembrane *status predicted
transmembrane *status predicted
extracellular *status predicted
hypervariable region HV2
transmembrane *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.; Heuer, I.; Meyer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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predicted predicted
                                                                                                                                                                                                                        <TM2>
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                                                                                                                                                                                                                                                                                                                              <MAT>
                                                                                                                                                                                                                                                                                                                                                   predicted
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                                                                                                          F;88-94/Domain: transmembrane #status predicted <TM3>
F;95-139/Domain: extracellular #status predicted <EXT2>
F;01-134/Region: hypervariable region HV1
F;140-154/Domain: transmembrane #status predicted <TM4>
F;160-170/Domain: transmembrane #status predicted <TM5>
F;171-217/Domain: extracellular #status predicted <EXT3>
F;176-223/Region: hypervariable region HV2
F;238-230/Domain: transmembrane #status predicted <TM6>
F;238-242/Domain: transmembrane #status predicted <TM7>
F;243-257/Domain: extracellular #status predicted <TM7>
F;243-257/Domain: extracellular #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1-10,11-23/Domain: signal sequence (fragments) #status F;24-266/Product: opacity protein opaD #status predicted F;34-42/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain MS11, variant 4.8 A; Experimental source: strain MS11, variant 4.8 A; Note: storession of openity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein
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S16616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: S16616
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C; Species: Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X52372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f \lambda; Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol.
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R; Bhat, K.S.; Gibbs, C.P.; Barrera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Variety: strain MS11
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Best Local
                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 TENQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTEVT
                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKVNGNRTDRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein opaD precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
ss: Neisseria gonorrhoeae
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                    76;
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                                                                                                                                                                                                                                                                                                                                                                                                                      semivariable region
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                    Conservative
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28.8%;
                                       29.0%;
                                                                   27.0%;
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               24;
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                                       Score 235;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O.; Morrison, S.G.;
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                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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                                                                 멂
                                         .4e-13;
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                                                                 2;
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                                                              Length 266;
               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <MAT>
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             90;
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             Gaps
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Nol. Microbiol. 5, 1889-1901, 1991

A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a famil A;Reference number: S16610; MUID:92114767

A;Accession: S16613

A;Accession: S16613
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S16613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: cell surface component; transmembrane protein F;1-13,14-104/Domain: signal sequence (fragments) #status F;105-338/Product: opacity protein opaB #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: the authors did not translate the sequence for the signal peptide A; Note: expression of opacity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opacity protein opaB precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                 F;315-329/Domain:
F;330-338/Domain:
                                                                                                                                                                                                                                                                                                                                                               F;182-207/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                    F;132-141/Region:
F;156-164/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;124-155/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-338 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X52373
                                                                                                                                                                                                                                                                                                        7;213-227/Domain: 1
F;224-289/Domain: 6
F;233-243/Domain:
                                                                                                                                                                                                                                                                                                                                                                                ;169-175/Domain:
;176-212/Domain:
                                                                                                                                                                                                                                                     306-314/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: cell surface component;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: opacity
                                                                                                                                                                                                                                                                                         249-295/Region:
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                        290-302/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
157 HPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTENQENGTFHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 AVTTYPQNAASSVTTNAPIRKLPHHESRSISSLGFGAVAGVGIDITPNLTLDAGYRYHNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 NIKTRKTEHRENGTFHAASSLGLSAVYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETI 185
                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
                                 47 SPRISAGYRINDLRFAVDYTRYK--NYKAPSTDFK-----
                                                                                                         10 ALALPAAALAEG-ASGFYVQADAAHA---
                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIKELLRNDNANSGGSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKALAALIALALPAAALAEG---ASGFYVQADAAHA-----KASSSLGS-
                                                                       SLLFAARAASEGNGRGPYVQADLAYAAERITHDYPEPTGAKKDKKSTVSDYFRNIRTHSI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTAPKKAQLSTVSD
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AKGFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                        hypervariable region HV1
transmembrane *status predicted
extracellular *status predicted
transmembrane *status predicted
                                                                                                                                                                                                                                                                                                                                                                                               transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                     semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                      extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane #status predicted
                                                                                                                                                                                                                   transmembrane #status
                                                                                                                                                                                                                                                                                         hypervariable
                                                                                                                                                                                                                                                                                                                                                                                  extracellular #status predicted
                                                                                                                                                                                                                                      extracellular
                                                                                                                                                                                                                                                     transmembrane
                                                                                                                                                                                                                                                                        transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                            27.0%;
                                                                                                                                         22;
                                                                                                                                                                                                                              #status predicted
#status predicted
#status predicted
                                                                                                                                                                                                                                                                                         region HV2
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                                                                                                                                                                             Score 234.5;
                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variant 4.8
                                                                                                                                             Mismatches
                                                                                                                                                                                                                 predicted
                                                                                                                                                              2e-13;
                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                     <TM7>
                                                                                                                                                                                                                                                                    <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <1M1>
                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                 <TM3>
                                                                                                         -KASSSLGS--
                                                                                                                                                                                                                   <8MT>
                                                                                                                                                                                                                                      <EXT4>
                                                                                                                                                                                                                                                                                                            <TM5>
                                                                                                                                                                                                                                                                                                                             <EXT3>
                                                                                                                                                                                                                                                                                                                                              <TM4>
                                                                                                                                                                                                                                                                                                                                                                                  <EXT2>
                                                                                                                                                                                                                                                                                                                                                                                                                      <TM2>
                                                                                                                                                                           Length
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
                                                                                                                                                                             338;
                                                                                                         --- AKGF 46
                                                                                                                                             87;
                                     J---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translated repeat
                                   80
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                                                                                                                                           9;
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Mol. Microbiol. 5, 1889-1901, 1991
A; Title: The opacity proteins of Neisseria A; Reference number: $16610; MUID: 92114767
A; Accession: $16612
A; Molecule +----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: opaE

C;Superfamily: opacity protein

C;Keywords: cell surface component; transmembrane protein

E;1-10,11-23/Domain: signal sequence (fragments) #status predicted (fragments) #status predicted (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain MS11, variant 4.8 A; Note: the authors did not translate the sequence for the signal peptide A; Note: expression of opacity proteins is regulated by the number of trans of repeats place the start codon in frame with the rest of the protein C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;95-131/Domain: extracellular #status predicted <EXT2>F;101-125/Region: hypervariable region HV1
F;132-146/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragments) (Species: Neisseria gonorrhoeae A;Variety: strain MS11 (C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;226-234/Domain: transmembrane #status predicted
F;235-249/Domain: extracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;152-162/Domain: transmembrane #status predicted F;163-209/Domain: extracellular #status predicted F;168-215/Region: hypervariable region HV2 F;210-222/Domain: transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;75-83/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;50-60/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;43-74/Domain: extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;34-42/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-258 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S16612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X52369
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250-258/Domain: transmembrane #status predicted
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                                                         126
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                                                                                                                                                                                                                                                                                                                                              2 KKALAALIALPAAALAEG---ASGFYVQADAAHA-----KASSSLGSAK-----
                                                      NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTEVTTI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEENTQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEAS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSLGLSAVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTKFLTSSYGGLNPTVY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS-----
                                                                                                            -----LYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS---- 124
                                                                                                                                                                        YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                                                                                                              -----GFSPRISAGYRINDLRFAVDYTRYK--NYKAPSTDFK------- 79
                                                                                                                                                                                                                                                                                       KKPSLLFSSLLFSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGVRYRF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.6e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 234;
-- AGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVN 156
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted <EXT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gonorrhoeae strain MS11 are encoded by a f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1M1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                    90;
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F;72-110/Domain: extracellular #status predicted <EXT2>
F;78-105/Region: hypervariable region HV1
F;111-125/Domain: transmembrane #status predicted <TM4>
F;131-141/Domain: transmembrane #status predicted <TM5>
F;131-141/Domain: extracellular #status predicted <EXT3>
F;142-188/Domain: extracellular #status predicted <EXT3>
F;147-194/Region: hypervariable region HV2
F;189-001/Domain: transmembrane #status predicted <TM6>
F;205-213/Domain: transmembrane #status predicted <TM7>
F;214-228/Domain: extracellular #status predicted <TM8>
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C;Keywords: cell surface component; transmembrane protein
C;Keywords: cell surface component; transmembrane protein
F;1-237/Product: opacity protein opa57 *status predicted <MAT>
F;1-19/Domain: transmembrane *status predicted <TMI>
F;20-51/Domain: extracellular *status predicted <EXTI>
                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;20-51/Domain:
F;28-37/Region:
F;52-60/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z18935; NID:g49331; PIDN:CAA79368.1; PID:g940797
A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;65-71/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: opa57
C;Superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-237 <KUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_rTitle: Variable opacity (Opa) outer membrane proteins account for the cell tropisms d A;Reference number: S36328; MUID:93178439 A;Accession: S36343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Kupsch,
EMBO J. 1
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C;Accession: S36343; S28626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Neisseria gonorrhoeae
A; Variety: strain_MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment) N; Alternate names: outer membrane protein opa57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                     236 RF 237
                                                                                                                                       173 KF 174
                                                                                                                                                                        177 QDAHRESDSIRRVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGVRY 235
                                                                                                                                                                                                                                    125
                                                                                                                                                                                                                                                                     121 AVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNT 176
                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                               61 DFGGWRIAADYARYRKWNNNKYSYSIKELLRNKGNGNRTDLKAENQENGTFHAVSSLGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                       55 RINDLRFAVDYTRYKNY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 NTR-FKTHEASLGVRYRF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 TVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 LHGPGTTPTVYPGKNTQDAHRESDSIRRVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 ALAEGASGFYVQADAAHA------KASSSLGS-----AKGFSPRISAGY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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12, 641-650, 1993
                                                                                                                                                                                                                   ------AGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRV 172
                                                                                                                                                                                                                                                                                                                     VIYDFDTQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASEDGGRGPYVQADLAYAYEHITHDYPEPTAPNKNKISTVSDYFRNIRTRSVHPRVSVGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.8%;
28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 68
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                                                                                                                                                                                                                                                                                                                                                                                                                  86
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C; Date:
                      C;Species: Neisseria gonorrhoeae
A;Variety: strain JS3
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A; Gene: opar
C; Superfamily: c
C; Keywords: cel
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F;132-146/Domain: transmembrane #status predicted <TM4>F;152-162/Domain: transmembrane #status predicted <TM5>F;163-208/Domain: extracellular #status predicted <EXT3>F;163-208/Domain: extracellular #status predicted <EXT3>F;163-209/Domain: transmembrane #status predicted <TM5>F;209-221/Domain: transmembrane #status predicted <TM6>F;225-233/Domain: transmembrane #status predicted <TM7>F;234-248/Domain: extracellular #status predicted <EXT4>F;249-257/Domain: transmembrane #status predicted <EXT4
opacity protein P.IIc precursor - Neisseria gonorrhoeae (strain JS3) (fragments) N:Alternate names: outer membrane protein P.IIc
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                                                                                                                                                             KONH2C
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F;75-83/Domain: transmembrane #status predicted <TM2>F;88-94/Domain: transmembrane #status predicted <TM3>F;88-94/Domain: transmembrane #status predicted 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOl. Microbiol. 5, 1889-1901, 1991
A;TitLe: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
A;Reference number: S16610; MUID:92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X52368
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A; Residues: 1-257 <BHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Nelsseria gonorrhoeae
A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Accession: S16614
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                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 VKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 SYGGLNPTVYTEENTQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLEN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTKFLTS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 YFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKALAALIALALPAAALAEG---ASGFYYQADAAHA-----KASSSLGSAK------
                                                                                                                                                                                                                                                                                                                                                                                                          TR-FKTHEASLGVRYRF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GFSPRISAGYRINDLRFAVDYTRYK--NYKAPSTDFK----------
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Pred. No. 1.8e-13;
""smatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 257;
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31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change

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C; Keywords: cell surface component; transmembrane protein F;1-10,11-23/Domain: signal sequence (fragments) #status predicted F;24-268/Product: opacity protein P.IIC *status experimental <MAT>F;34-42/Domain: transmembrane *status predicted <TML>F;43-74/Domain: extracellular *status predicted <EXT1>F;51-60/Region: semivariable region
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A;Note: 241-Val was also found
A;Note: expression of opacity proteins is regulated by the number of translated
of repeats place the start codon in frame with the rest of the protein
R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wol. microbiol. 2, 797-806, 1988
A;Title: Three copies of a single protein II-encoding sequence in the genome of Neisser: A;Reference number: S03095; MUID:89096501
A;Accession: S03095
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R;van der Ley, P.
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F;101-135/Region: hypervariable region HV1
F;141-155/Domain: transmembrane #status predicted <TM4>
F;161-171/Domain: transmembrane #status predicted <TM5>
F;161-171/Domain: extracellular #status predicted <EXT3)
F;172-25/Region: hypervariable region HV2
F;202-232/Domain: transmembrane #status predicted <TM6>

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A;Title: Antigenic and structural differences among six proteins II expressed by a sing
A;Reference number: S16360; MUID:87306843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F; 51-60/Region: F; 75-83/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;88-94/Domain: transmembrane #status predicted <TM2>F;88-94/Domain: transmembrane #status predicted <TM3>
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opacity protein-related protein OPM1 precursor - Neisseria meningitidis (strain C1938)
N;Alternate names: outer membrane protein class 5
C;Species: Neisseria meningitidis
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F;260-268/Domain:
                                                                                                                                        S08514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: opacity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-268 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260-268/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                     253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AALIALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAK-----
                                                                                                                                                                                                                                                                                                                     TR-FKTHEASLGMRYRF 268
                                                                                                                                                                                                                                                                                                                                                                                                       VKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GGSDSFSK-----TSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEHQENGTFHAVSSLGLSTIYDFDTGSRFKPYIGMRVAYGHVRHQVRSVEQETEIITTYP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSVHPRVSVGYDFGSWRIAADYARYRKWNNNKYSVSIKELLRNDNSASGVRGHLNIQTQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLLFSSAARAASEDGGRGPYVQADLAYAAERITHDYPKPTGTGKNKISTVSDYFRNIRT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDFK------LYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NYKAPS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 68
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A;Variety: strain C1938
C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
C;Accession: S08514
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C;Accession: $08514
R;Stern, A.; Meyer, T.F.
R;Stern, A.; Meyer, T.F.
R;Stern, A.; Meyer, T.F.
R;Stern, A.; Meyer, T.F.
opacity protein opaC precursor - Neisseria gonorrhoeae (strain MS11) (fragments) N; Alternate names: opacity protein V0; triosephosphate dehydrogenase C; Species: Neisseria gonorrhoeae A; Variety: strain MS11
C; Date: 31-Mar:1989 #sequence_revision 17-Oct-1997 #text_change 16-Jul-1999
C; Accession: S16618; A24429; S36328; S28621
C; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc Mol. Microbiol. 5, 1889-1901, 1991
A; Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fa; Reference number: S16610; MUID:92114767
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F;130-144/Domain: transmembrane *status predicted <TM4>F;150-160/Domain: transmembrane *status predicted <TM5>F;161-209/Domain: extracellular *status predicted <EXT3>F;161-209/Domain: hypervariable region HV2
F;210-222/Domain: transmembrane *status predicted <TM6>F;210-222/Domain: transmembrane *status predicted <TM6>F;210-223/Domain: transmembrane *status predicted <TM6>F;210-23/Domain: transmembrane *status predicted <TM6>F;210-23/Domain: transmembrane *status predicted <TM6>F;210-23/Domain: transmembrane *stat
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A;Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein
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A; Residues: 1-258 <STE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 SSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPKGGTPAGGPVIK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 GVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 FSPRISAGYRINDLRFAVDYTRYK-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 IHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKTEHOGNGSFHAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LIALALPAAALAEGASGFYVQADAAHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDPSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMRYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSIGASVIYDFDTQSPVKPYFGARLSLNR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFSSAAQAASEDGSRSPYYVQADLAYAAERITHNYPEPTGADKDKISTVSDYFRNIRAHS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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28.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 231; DB 2
Pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigenic variation in pathogenic nei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <8MT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ASAHLGGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #status
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F;76-84/Domain: transmembrane #status predicted <TM2>
F;89-95/Domain: transmembrane #status predicted <TM3>
F;89-95/Domain: extracellular #status predicted <EXT2>
F;102-129/Region: hypervariable region HV1
F;135-149/Domain: transmembrane #status predicted <TM4>
F;155-165/Domain: transmembrane #status predicted <TM5>
F;166-211/Domain: extracellular #status predicted <EXT3>
F;167-11/Region: hypervariable region HV2
F;171-217/Region: hypervariable region HV2
F;28-236/Domain: transmembrane #status predicted <TM6>
F;28-236/Domain: transmembrane #status predicted <TM6-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: cell surface component; transmembrane protein F;1-11,12-24/Domain: signal sequence (fragments) #status predicted <SIG>F;25-260/Product: opacity protein opac #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Meyer, T.F. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: opaC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 25-260 <MEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S28621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Variable opacity (Opa) outer membrane proteins account for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F. EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: this protein is synthesized as a precursor; however,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variati
A;Reference number: A90887; MUID:87002493
A;Accession: A24429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X52370
A;Experimental source: strain MS11, variant 4.8
A;Experimental source: strain MS11, variant 4.8
A;Note: the authors translated the codon CCA for residue 32 as Thr
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
A;Stern, A;Brown, M; Nickel, P; Meyer, T.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S16618
A; Molecule type: DN
A; Residues: 1-260 <
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A; Residues: 25-260 <KUP>
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Keywords: cell surface compo
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107 ---LNRASAHLGGSDSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRS 163
                                                                         134 SFHAVSSLGLSAIYDFQINDKFKPYIGARVAYGHVRHSIDSTKKITGLLTTSTPGIMSGV 193
                                                                                                                                                                                                                                 74 HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENG 133
                                                                                                                                                                    78 -- FKLYSIGASVIYDFDTQSPVKPYFGARLS----
                                                                                                                                                                                                                                                                                                                    14 SSLLFSSAAQAASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AALIALALPAAALAEGASGFYVQADAAHA-----KASSSLGSAKGFS------
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Pred. No. 3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
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F:156-170/Domain: transmembrane #status predicted <TM4>
F:176-186/Domain: transmembrane #status predicted <TM5>
F:187-234/Domain: extracellular #status predicted <EXT3.
F:192-240/Region: hypervariable region Hv2
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R;Waldbeser, L.S.; Ajioka, R.S.; Merz, A.J.; Puaoi, D.; Lin, L.; Thomas, M.; So, M. Mol. Microbiol. 13, 919-928, 1994

A;Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell A;Reference number: $72343; MUID:95115561

A;Accession: $72343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1-48/Domain: signal sequence #status predicted <SIG>F;49-283/Product: opacity protein opaH #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: cell surface component; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: expression of opacity proteins is regulated by the number of to repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U13708; NID:g535357; PIDN:AAA74082.1; PID:g535358
A;Experimental source: isolate 15063G
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063g) N;Alternate names: cell invasion protein opaH C;Species: Neisseria gonorrhoeae A;Variety: isolate 15063G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: opacity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-283 <WAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S72343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251-259/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235-247/Domain:
276 SLGMRYRF 283
                                                   167 SAGVRVKF 174
                                                                                         217 DIGPKTQDAHQESNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEA 275
                                                                                                                                                                                          161 SLGLSAVYDFKLNDKFKPYIGARV----AYGHVRHSIDSTKKTTKILTSFYGVATKPTTY 216
                                                                                                                                                                                                                                                                                           101 PRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIERVQEAHSNRIDLKAENQENGTFHAVS 160
                                                                                                                                                                                                                                                82 SIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS---------
                                                                                                                                                                                                                                                                                                                                              41 SLLSAAQAASEAMRGPYVQADLAFAAERITHDYPEPTGTKKGTISTVSDYFRNIRTHSVH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 HEASLGVRYRF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 YKVLRTPGAH---RESDSIRRVGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ALALPAAALAEGASGFYYQADAAHAKA-----SSSLGSAKG------FS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
                                                                                                                                         -----AGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGEL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane #status predicted transmembrane #status predicted extracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.6%; Score 231; DB 2; 28.2%; Pred. No. 3.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <8MT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <EXT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
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C;Species: Neisseria gonorrhoeae
A;Yariety: strain MS11
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
C;Accession: S16617; S36332; S28618; S28622; S36333
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami A;Reference number: S16610; MUID: 92114767
A;Reference number: S16610; MUID: 92114767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 39-248; 'N', 250-282 <KUP>
A; Residues: 39-248; 'N', 250-282 <KUP>
A; Cross-references: EMBL:Z18931; NID:g49327; PIDN:CAA79364.1; PID:g940793; EMBL:Z18932;
A; Experimental source: strain MS11, variant F3
A; Experimental source: strain MS11, variant F3
A; Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain MS11, varaint 4.8
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat 6
of repeats place the start codon in frame with the rest of the protein
R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
A;Reference number: S36328; MUID:93178439
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C;Species: Neisseria concrrhoman
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C;Keywords: cell surface component; transmembrane protein
F;1-15,16-38/Domain: signal sequence (fragments) #status predicted <SIG>
F;39-282/Product: opacity protein opal #status predicted <MAT>
F;49-57/Domain: transmembrane #status predicted <TM1>
F;58-89/Domain: extracellular #status predicted <EXTI>
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A; Residues: 1-282 <BHA>
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F;234-246/Domain: transmembrane #status predicted <PMS>F;234-246/Domain: tran
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F;156-170/Domain: transmembrane #status predicted <TM4>F;156-170/Domain: transmembrane #status predicted <TM4>
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F;90-98/Domain: transmembrane #status predicted <TM2>
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           160 NVRSGELSAGVRVKF 174
                                                                                                              209 NAASSVTTNAPIRKLPHHESRSISSLGFGAVAGVGIDITPKLTLDAGYRYHNWGRLENTR 268
                                                                                                                                                                                                                                                                                                                               149 EHRENGTFHAASSLGLSAVYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETIAVTTYPQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 SIHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVNIKELLRNDNANSGGNKHLNIKTRKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 GFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 SLLFPSAAQAAGEGNGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSDYFRNIRTH 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ALALPAAALAEG---ASGFYVQADAAHA-----KASSSLGSAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  DFK------LYSIGASVIYDFDTQSPVKPYFGARLSL--
                                                                                                                                                                                                                      NRASA-----HLGGSDSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVK 159
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#status predicted <TM7>
#status predicted <EXT4:</pre>
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Pred. No. 5.6e-13;
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: | | | | : | Db 269 -FKTHEASLGVRYRF 282

Search completed: October 28, 2002, 16:03:37 Job time: 13.4821 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Transmembrane; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria gonorrhoeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEIN SERVES AS A PORIN. SUBUNIT: HOMOTRIMER.
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                                                                                                                                               AALIALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAK------
                                                                               SSLLFSSAARAASEDGGRGPYVQADLAYAAERITHDYPKPTGTGKNKISTVSDYFRNIRT
       -GFSPRISAGYRINDLRFAVDYTRYK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X12625; CAA31144.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
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26.5%;
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Last annotation update)
n P.IIC precursor (Protein
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                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                Score 233.5;
Pred. No. 3.
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                                                                                                                                                                                                                    Mismatches
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nes 71;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup C).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Common mechanism controlling phase and antigenic variation pathogenic neisseriae.";
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                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=135720;
                                                                                                                                                                                                                                                                                                        Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                     EMBL; X06445; CAA29748.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88260884; PubMed=2455211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 VKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 ---GGSDSFSK------TSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                                                                          InterPro; IPR003394; Opacity.
   115
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   GGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGIONS OF HOMOLOGY WITH N.GONORRHOEAE (STRAIN MS11) OPA GENE
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                            EHQGNGSFHATSSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPK 184
                                                                                                                                                     KTFSSLLFSSLLFSSAAQAASEDGSRSPYYVQADLAYAAERITHNYPEPTGADKDKISTV 64
                                                                                                                                                                                  KALAALTALALPAAALAEGA-----SGFYVQADAAHA------KASSSLG 41
                                                                                                                                                                                                                                                                                                                                        S08514; S08514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiol.
                                                         DFK-----LYSIGASVIYDFDTQSPVKPYFGARLSLNR--
                                                                                          SDYFRNIRAHSIHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKT
                                                                                                                         S-----AKGFSPRISAGYRINDLRFAVDYTRYK----
                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 10,
(Rel. 10,
(Rel. 40,
                                                                                                                                                                                                                                                                             260 AA;
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:5-12(1987)
                                                                                                                                                                                                                                                                             28936 MW; EB47A2843B3F037B CRC64;
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 -DSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNT 157
                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                             Score 232; DB 1;
Pred. No. 4.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPACITY-RELATED PROTEIN POPM3 AND
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l. Usage by ar
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                                                                                                                         --NYKAPST 76
                                                               ----ASAHL 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
0pacity protein OPA67 precursor (Fragment).
Meisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epithelial cells.";
EMBO J. 12:641-650(1993).
-I- FUNCTION: INPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the c
tropisms displayed by Neisseria gonorrhoeae for human leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _NEIGO
OP67_NEIGO
                                                                                                                                                                                                                                                                                                                                                                         Outer
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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         178
                                    125
                                                                122 LNDKFKPYIGARV---
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                                                                                             93
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                                                                                                                                                     5
                                                                                                                                                                                                    19 AEG-ASGFYVQADAAHA------KASSSLGSAKGF-----SPRISAGY 54
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Outer membrane.
ESNSIRRYGLGVIAGVGFDITFNLTLDAGYRYHNWGRLENTR-FKTHEASLGVRYRF 233
                         -----AGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                       TQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS--------------
                                                                                                               DFGGWRIAADYARYRKWNNSKYSVSIKKLQNQYNKKTENQENGTFHAASSLGLSAVYDFK 121
                                                                                                                                                  RINDLRFAVDYTRYKNY----
                                                                                                                                                                         SEGNGRGPYVQADLAYAAERITHDYPEATAQKKGTTISTVSDYFRNIRTHSVHPRVSVGY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                 S28625; S28625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                            Z18942; CAA79375.1; -.
                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                     Similarity
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233
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                           >233
233
                                                                                                                                                                                                                                                                                               26039 MW;
                                                                                                                                                                                                                                                    26.0%;
27.8%;
                                                        AYGHVRHSIDSTKKTTGFLTTAGARGAAPTVSSPYKNTQDAHQ 177
                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                Score 226;
                                                                                                                                                                                                                                                                                                                          OPACITY PROTEIN OPA67.
                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                              -----KAPSTDFKLYSIGASVIYDFD 92
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                                                                                                                                                                                                                                                                                            6C13A46AB163C67F CRC64;
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                                                                                                                                                                                                                                                 ; DB 1; Length 233;
1.4e-13;
                                                                                                                                                                                                                                      58;
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OPAJ_NEIGO
ID OPAJ_NEIGO
AC Q04882;
DT 01-OCT-1993
DT 01-OCT-1993
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPAB_NEIGO STANDARD; PRT; 234 AA Q04874; O1-OCT-1993 (Rel. 27, Created) O1-OCT-1993 (Rel. 27, Last sequence update) O1-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S28628; S28628.
PIR; S36329; S36329.
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Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the ctropisms displayed by Neisseria gonorrhoeae for human leukocytes epithelial cells.";
epithelial cells.";
EMBO J. 12:641-650(1993).
-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z18928; CAA79361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Opacity protein
                                                                                                                             178 HOSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                  122
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                                                                                                                                                                                                                                                                                                                                                       19 AEG-ASGFYYQADAAHA-----KASSSLGSAK------GFSPRISAGYR 55
                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                        56 INDLREAVDYTRYK--NYKAPSTDFK------------LYSIGASVIY 89
                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                        2 SEGNGRGPYVQADLAYAYEHITHDYPEQTGTKKDKISTVSDYFRNIRTHSIHPRVSVGYD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                        DFKLNGKFKPYIGARV----AYGHVRHSIDSTKKTTKFLTSSYGGLNPTVYTEENTQNAH
                                                                                                                                                                                                                                                        FGGWRIAADYARYRKWNDNKYSVDIKELENKNQNKRDLKTENQENGTFHAVSSLGLSAVY 121
                                                                                                                                                         ------AGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                            DFDTQSPVKPYFGARLSLNRASAHLGGS-DSFSKTS-----
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                                                STANDARD;
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234
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26772 MW; 9FFE5B5DABBA96CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       25.9%; Score 225.5; DB 1; Length 234; 29.0%; Pred. No. 1.6e-13;
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                                              PRT;
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(Rel. 27, Created)
(Rel. 27, Last sequence update)

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SQUE TET TWEET TO COLOR 
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"Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells.";
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                                                                                                                                                    Q04878;
01-OCT-1993 (Rel. 27,
01-OCT-1993 (Rel. 27,
01-NOV-1995 (Rel. 32,
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NCBI_TaxID=485; [1]
                                               Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                       Opacity protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                        125
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
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                                                                                                                                                                                                                                                         NEIGO
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237
237 AA;
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OPA58 precursor (Fragment).
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                                                     beta subdivision; Neisseriaceae; Neisseria
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Pred. No. 1.
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Q04879;
01-OCT-1993
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no warmodified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelial cells.";
EMBO J. 12:641-650(1993).
-i-FUNCTION: IMPLICATED IN A NUMBER
PROTEINS ARE IMPLICATED IN PATHOG
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Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.; "Variable opacity (Opa) outer membrane proteins account for the ctropisms displayed by Neisseria gonorrhoeae for human leukocytes epithelial cells.";
                                                           SEQUENCE FROM N.A.
STRAIN-MS11 / F3;
MEDLINE-93178439; PubMed-8440254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003394; Opacity. Pfam; PF02462; Opacity; 1.
                                                                                                                     NCBI_TaxID=485;
                                                                                                                                       Bacteria;
                                                                                                                                                   Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                               --AGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                          PVKPYFGARLSLNRASAHLGGS-DSFSKTS----
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                                                                                                                                       gonorrhoeae.
Proteobacteria;
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(Rel. 27, Last seq
(Rel. 32, Last ann
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                                                                                                                                                                                                                                                            STANDARD;
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Pred. No. 1.7e-13
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PATHOGENESIS AND ARE SUBJECT
                                                                                                                                       subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 234;
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Best Local
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01-JUL-1989
01-NOV-1995
STRAIN-MS11 / F3;

MEDLINE-93118439; PubMed-8440254;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

"Variable opacity (Opa) outer membrane proteins account fo

tropisms displayed by Neisseria gonorrhoeae for human leuk
                                                                                                                                                                                                                                         "Opacity genes in Neisseria gonorrhoeae: antigenic variation.";
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN-MS11 / V0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Opacity protein OPA50 precursor (OPA30) (V0) (Fragment).
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             MEDLINE=87002493; PubMed=3093085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria gonorrhoeae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-485;
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FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
DECOMPTINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; beta subdivision; Neisseriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11, Last sequence update)
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                                                                                                                                                                                                                                                                                                                   Nickel P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26868 MW; 5175C6606839EFFB CRC64;
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                                                                                                                                                                                                                                                                                                                Meyer T.F.;
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OPAH_NEIGO
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EMBL; Z18927; CAA79360.1; -.
PIR, A24429; KONHO.
PIR; S28621; S28621
PIR; S28621; S28621
PIR; S36328; S36328
InterPro; IPR003394; Opacity.
Pfam; PF02462; Opacity; 1.
                                     SEQUENCE FROM N.A.

STRAIN-MS11 / F3;

MEDLINE-93178439; PubMed-8440254;

Kupsch E.-M., Knepper B., Kuroki T., Heuer I., M.

"Variable opacity (Opa) outer membrane proteins of tropisms of displayed by Neisseria gonorrhoeae for epithelial cells.;

EMBO J. 12:641-650(1993).
                                                                                                                                                                                                                                                                                                                   Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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15-DEC-1998
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01-OCT-1993
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EMBO J. 12:641-650(1993).
-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
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236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   precursor (Fragment).
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                                                                                        outer membrane proteins account for the cell elseria gonorrhoeae for human leukocytes and
                                                                                                                                              Kuroki T., Heuer I., Meyer T.F.;
                                                                                                                                                                                                                                                                                                                 beta subdivision; Neisseriaceae; Neisseria
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MEDLINE=92114767; PubMed=1815562;
Q04885;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1995 (Rel. 32, Last annotation updat
01-NOV-1995 (Rel. 32, Last annotation updat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA;
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238
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                                                                                       STANDARD;
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OPACITY PROTEIN OPAGO.

SED -> MLKA (IN MS11 / V18).

V -> M (IN MS11 / V18).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93178439; PubMed=8440254;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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01-NOV-1995
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STRAIN=MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
                            SEQUENCE FROM N.A.
                                                                      Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                  OPAD
                                                                                                           Opacity protein OPA59
                                                                                                                                                    01-OCT-1993
                                                                                                                                                                   Q04883;
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                                                      NCBI_TaxID=485;
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FUNCTION: IMPLICATED IN
PROTEINS ARE IMPLICATED
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                                                                                                                                                                                                                                                                                                                                                                                       AVDYTRYK----
                                                                                                                                                                                                                                                   FGAMAGYGIDVAPGLTLDAGYRYHYWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                                                                           LGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                  VKPYFGARLSLNRASAHL-----
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234 AA;
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(Rel. 27, Last sequence update)
(Rel. 32, Last annotation update)
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                                                                                                                                                                                STANDARD;
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OPACITY PROTEIN OPA65
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                                                                       Neisseriaceae; Neisseria
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RESULT 13
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Best Local
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Q04877;

01-OCT-1993 (Rel. 27, Created)

01-OCT-1993 (Rel. 27, Last seque

01-NOV-1995 (Rel. 32, Last annot)

Opacity protein OPA54 precursor
                                                STRAIN-MSI1 / F3;
STRAIN-MSI1 / F3;
MEDLINE-93178439; PubMed-8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., M
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., M
Variable opacity (Opa) outer membrane proteins

"Variable opacity (Opa) outer membrane proteins
epithelial celis.";

epithelial celis.";

EMBO J. 12:641-650(1993).

-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.

-I- FUNCTION: TARTE TARTE IN PARHOGENESIS AND ARE SUBJECT
                                                                                                                                                                         Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OF PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the openions displayed by Neisseria gonorrhoeae for human leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              DSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                       VYDFDTGSRFKPYIGMRVAYGHVRHQVRSVQQETIAVTTYPQNAASSVTTNAPIRKLPHH 187
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Last annotation updat
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Pred. No. 4.
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                                                                                                                                                                                                                                (Fragment).
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                                                          Heuer I., Meyer T.F.; ne proteins account for the arrhoeae for human leukocytes
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                                                                                                                                                                               MEDILINE-8700249; PubMed-3093085;
Stern A., Brown M., Nickel P., Meyer T.F.;
"Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation.";
Cell 47:61-71(1986).
-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS.
-PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Opacity protein V28 precursor (Fragment).
Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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                                   the European Bioinformatics Institute.
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                                                                                                                                               -!- SUBCELLULAR LOCATION: Outer membrane.
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Pfam; PF02462; Opacity; 1.
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           non-profit
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244 AA;
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                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OVT-1995 (Rel. 32, Last annotation updato)
Opacity protein OPA66 precursor (Fragment).
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                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial cells.";
EMBO J. 12:641-650(1993).

-i- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OP
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO
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Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
"Variable opacity (Opa) outer membrane proteins account for the c
tropisms displayed by Neisseria gonorrhoeae for human leukocytes
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Q9rp16 neisseria m
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Best Local Similarity 100.
Matches 174; Conservative
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                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                      MEDLINE-99270944; PubMed-10338491; Plante M., Cadieux N., Rioux C.R., Har **RANTIGE** Annityenic and molecular conservation
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-B2
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                           Infect. Immun. 67:2855-2861(1999).
EMBL; U52069; AAB41581.1; -.
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 121 SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
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                           FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                                                                     {\tt MKKALAALIALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR}
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174 AA; 18337 MW;
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                                       Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
                                                                                                                                        STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                  Martin D., Cadieux N., H
Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis, and
Neisseria meningitidis (sero
Bacteria: Proteobacteria; be
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01-DEC-2001 (TrEMBLrel. 19, Last annotation
OUTER MEMBRAGE PROTEIN PRECURSOR.
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01-MAY-1997 (TERMBLrel. 03, Created)
01-MAY-1997 (TERMBLrel. 03, Last seq
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                        Rajandream M.A., Rutherford K.M.,
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 STRAIN-Z4063;
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EMBL; AF175676; AAD53279.1; -. InterPro; IPR003394; Opacity.
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174 AA; 18357 MW;
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Barrell B.G.;
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EMBL/GenBank/DDBJ
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subdivision;
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                         "Differences in Surface Expression of Neisserial Surface Protein among Neisseria meningitidis Group B strains."; Infect. Immun. 0:0-0(1999).

EMBL; AF175681; AAD53284.1; -. InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                                                                           STRAIN=NG3/88;
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Bacteria; Proteobacteria;
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SIGNAL 1 19
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EMBL; AL163754; CAB84143.1; --
InterPro; IPR003394; Opacity.
Pfam; PF02462; Opacity; 1.
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                                     FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                                                                                                       MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                 165;
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18355 MW;
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95.48;
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13,
17,
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                                                                                                                                                                         Score 832;
Pred. No. 1.
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Pred. No. 8.5e-61;
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                                                                                                                                                                                                       ECF6F38B9286800E CRC64;
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01-MAY-2000
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                      Q9R2R1;
01-MAY-2000 (TIEMBLIEL 13,
01-MAY-2000 (TIEMBLIEL 13,
01-JUN-2001 (TIEMBLIEL 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect.
   SEQUENCE FROM N.A.
STRAIN=M136, AND B2232;
MOE G.R., Tan S., Granoff D.M.;
"Differences in Surface Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMcd-10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis, and
Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SURFACE PROTEIN A (OUTER MEMBRANE NSPA OR NMB0663.
                                                                                                                                                                                                                 Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                              NSPA.
                                                                                                                                                                                                                                                                                                                            SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R2R1
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EMBL; AF175678; AAD53281.1;
EMBL; AE0024420; AAF41081.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CU385;
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                                                                                                                                                                            CBI_TaxID=487;
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94.8%;
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Group B strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 829; DB 16;
Pred. No. 2.2e-60;
                                                                                                                                                                                                                 subdivision; Neisseriaceae; Neisseria
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subdivision;
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01-MAY-1997 (TYEMBLITEL. 03, Last sequence update)
01-JUN-2001 (TYEMBLITEL. 17, Last annotation updat
OUTER MEMBRANE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infect. Immun. 0.0-0(1999).
EMBL; AR175679; AAD53280.1; -.
EMBL; AF175677; AAD53280.1; -.
InterPro; IPR003394; Opacity.
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                          Signa.
                                                                                                                                                                                                                                                                                             Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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"Costimulation of T cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97149429; PubMed=8996237;
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"Differences in Surface Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CD47) is an adhesion-dependent, CD28-independent signaling.
J. Exp. Med. 185:1-11(1997).
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ct. Immun. 0:0-0(199).
; U52066; AAC36000.1; -.
; AF175683; AAD53286.1; -.
AF175682; AAD53285.1; -.
Pro; IPR003344.
                                                                      MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                            MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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18425 MW;
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                                                                                                                                      Mismatches
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                                                                                                                                                           No. 4.6e-60;
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.6e-60;
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Best Local
                                                                                                                                                                                                                  051124 PRELIMINARY; PRT; 256 AA.
051124;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
        Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B., Heckels J.E., Cannon J.G., Achtman M.; Recombinational reassortment among opa genes from ET-37 complex Microbiology 144:157-166(1998).

EMBL; U37255, AAC46101.1; -.

EMBL; U37255, AAC46101.1; -.

InterPro, IPR003394; Opacity.
                                                                                                                                                                       Neisseria meningitidis
Bacteria; Proteobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directed against Neisseria meningitidis Infect. Immun. 67:4955-4959(1999). EMBL; U52067; AAB41579.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
OUTER MEMBRANE PROTEIN PRECURSOR.
                                                                                                   MEDLINE=98129089; PubMed=9467908;
                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.; "Bactericidal and cross-protective activities of a monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=487;
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PF02462;
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175 AA;
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Opacity;
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18572 MW;
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93.7%;
                                                                                                                                                                      beta subdivision; Neisseriaceae; Neisseria.
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Dlea8F2FF5CC2FEA CRC64;
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                                                                                                                                              Query Match
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                                                                                                                                                                                                                                      Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz B. Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S., Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; "Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF001194; AAC32715.1; -.

EMBL; AF002194; CAC33638.1; -.

EMBL; PF02462; Opacity; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R719;
01-MAY-2000
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               years of epidemic spread.";
Mol. Microbiol. 25:1047-1064(1997)
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                                         AALAEGA-SGFYVQADAAH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIALALPAAALAEGASGFYVQADAAHA------KASSSLGS-----AKGFS 47
AASEDGSRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHSIHPRVSVGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGASVIYDFDTQSPVKPYFGARLSLNR-------ASAHLGG-----
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                                                                                                                       Similarity
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                                                                                                                                                                                               234 AA;
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                                                                                                          Score 237; DB 2,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                               F97142F463136EC1 CRC64;
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                                           -----AKASSSLGS-----AKGFSPRISAGY 54
                                                                                             Mismatches
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Best Local
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Q9R7I8;
Neisseria meningitidis.
Bacteria; Proteobacteria; beta
NCBI_TaxID=487;
                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, OPACITY PROTEIN (FRAGMENT).
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Mol. Microbiol. 25:1047-1064(1997).
EMBL; AF001195; AAC32716.1;
InterPro; IRR003394; Opacity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDFKLSDKFKPYIGVRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDFDTQSPVKPYFGARLSLNR-------ASAHLGG------SDSFSK 122
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Pred. No. 7
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Best Local
                          Matches
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Best Local :
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01-JUL-1997
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Achtman M.;
Achtman M.;
Achtman M.;
Achtman M.;
Clonal descent and microevolution of Neisseria meningitidis during years of epidemic spread.";
Mol. Microbiol. 25:1047-1064(1997).
EMBL; AF001196; AAC32717.1;
EMBL; AF001196; CAC32717.1;
InterPro; IPR003394; Opacity.
                                                                                                            years of epidemic spread.";

Mol. Microbiol. 25:1047-1064

Mol. Microbiol. 25:1047-106;

EMBL; AF001204; AAG32725.1; -.

EMBL; AF004823; AAG32684.1; -.

InterPro; IPR003394; Opacity.
                                                                            SEQUENCE
                                                                                                InterPro; IPR003394; Opaci
Pfam; PF02462; Opacity; 1.
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                                                                                                                                                                                         del Valle J., Achtman M.;
                                                                                                                                                                                                    Morelli G., Malorny B.,
                                                                                                                                                                                                                 MEDLINE=98010345; PubMed=9350862;
                                                                                                                                                                                                                                 STRAIN=Z3915
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
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                                                                                                                                                                           "Clonal descent and microevolution
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=487;
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SEQUENCE FROM N.A.
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16 AALAEGA-SGFYVQADAAHA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                       ITY PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RINDLRFAVDYTRYK-----NYKAPSTDFK--------LYSIGASVI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDFKLNDKFKPYIGVRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDFDTQSPVKPYFGARLSLNR------ASAHLGG-----SDSFSK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                    M., Malorny B., ed (JUN-1997) to
                                      Similarity
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                                                                        234 AA; 25933 MW; 61E3755DDE82AFE2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA;
                         Conservative
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                                     27.0%; Score 235; 28.0%; Pred. No. 1
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                                                                                                                                                                                                     Mueller K.,
                                                                                                                                                                                                                                                                   Morelli G.;
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                               beta subdivision; Neisseriaceae;
                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
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                         Mismatches
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                                                                                                                                                                                                   Seiler A., Wang J.-F.,
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                                  5; DB 2;
1.1e-11;
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                      74;
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                     Gaps
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RESULT
ID 125
ID 25
ID 25
ID 25
ID 27
ID 2
  RESULT 15
Q9R9A7
ID Q9R9A
AC Q9R9A
DT 01-MA
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Q51125;
Q1-NOV-1996
Q1-NAY-1997
Q1-MAY-1997
Q1-JQN-2001
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01-MAY-1997 (TremBLrel. 03, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
Q9R9A7;
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98129089; PubMed-9467908;
Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecck B.,
Heckels J.E., Cannon J.G., Achtman M.;
"Recombinational reassortment among opa genes from ET-37 complex
Neisseria meningitials isolates of diverse geographical origins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                       Q9R9A7
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EMBL; U37256; AAC46102.1; -.
InterPro; IPR003394; Opacity.
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NON_TER 1 1
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                                                                                                                                                                                                                                                                                                    TDPSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSL
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                                                                                                                                                                                             GMRYHF 259
                                                                                                                                                                                                                                                                                                                                  -----SDSFSKTSAGLGVLAGYSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSÅ 168
                                                                                                                                                                                                                                                                                                                                                                                                        SSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPTATSPQGGPIIQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHPRVSVGYDFGDWRIAADYASYRKWKESNSSTNAENRDNAKNYVKIETKHQGNGSFHAA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SIGASVIYDFDTQSPVKPYFGARLSLNR----
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                                                          PRELIMINARY;
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28.5%;
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     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ASAHLGG----
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                                                                                                                                                                                                                                                                                                                                                                            years of epidemic spread.";
Mol. Microbiol. 25:1047-1064(1997).
EMBL; AF031337; AAC45980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98010345; PubMed=9350862;
MORTELLI G., Malorny B., Muller K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) OPACITY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Achtman M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                 [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                          Clonal descent and microevolution of Neisseria meningitidis during 30
188
                           131 AGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                            128
                                                                                            97
                                                                                                                         68 ADYASYRKWKESNYSKKYTEFKHQNGNKQEDKTEHQGNGSFHATSSLGLSAIYDFKLNDK 127
                                                                                                                                                       63
                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                    23 SGFYVQADAAH------AKASSSLGS-----AKGFSPRISAGYRINDLRFA 62
                                                                                                                                                                                      8 SPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHSIHPRVSVGYDFGDWRIA 67
                                                                                          VKPYFGARLSLNR------ASAHLGG-----SDSFSKTSAGLGVL 130
AGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGMRYHF
                                                         FKPYIGVRVAYGHVKHQVHSVESKTTTVTTNNGGPVPQGPTPKPAYHESHSISSVGLGVI
                                                                                                                                                       VDYTRYK-----NYKAPSTDFK---
                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                            IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                 230 AA;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                 25819 MW;
                                                                                                                                                                                                                                                                  26.8%; Score 233.5; DB 2 28.6%; Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                 970DC4570B57A697 CRC64;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seiler A., Wang J.F., del Valle J.,
                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                        ----LYSIGASVIYDFDTQSP
                                                                                                                                                                                                                                                      60; Indels
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7;

Search completed: October 28, 2002, 16:02:40 Job time: 20.9713 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein -
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9
                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
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                                                                                                                                                                                                                                               Query
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/cgn2_6/ptodata/1/paa/US06_COMB.pep: *
/cgn2_6/ptodata/1/paa/US081_COMB.pep: *
/cgn2_6/ptodata/1/paa/US081_COMB.pep: *
/cgn2_6/ptodata/1/paa/US081_COMB.pep: *
/cgn2_6/ptodata/1/paa/US082_COMB.pep: *
/cgn2_6/ptodata/1/paa/US083_COMB.pep: *
/cgn2_6/ptodata/1/paa/US086_COMB.pep: *
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/cgn2_6/ptodata/1/paa/US092_COMB.pep: *
/cgn2_6/ptodata/1/paa/US093_COMB.pep: *
/cgn2_6/ptodata/1/paa/US093_COMB.pep: *
/cgn2_6/ptodata/1/paa/US096_COMB.pep: *
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Copyright (c) 1993 - 2002 Compugen Ltd
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          3 US-08-406-362-2
2 US-09-870-759-36
3 US-08-479-520-20
3 US-08-486-050-20
3 US-08-486-050A-20
13 US-08-988-444-20
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Sequence 2, Appli
Sequence 36, Appl
Sequence 20, Appl
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10.1	10.3		11.2 11.2 10.9 10.9 10.9	14.9 14.9 13.1 12.6 11.6 11.6
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223322	8 1 2 2 2 4 8 ¢	24 24 24 24	10 10 10 10 10 10	18 22 19 18 19 24 26
-08-467-722- S-09-451-184 S-09-902-540 S-09-952-267 S-09-952-267 S-09-952-267 S-09-952-267 S-09-952-267	A-745 -7 -7 -7 -3 A-3 A-3	-10-015-127-13821 -09-540-236-2792 -60-128-476-4082 -USO2-03987-13845 -09-815-242-13845	-691C-91 -014-123 -618-47 3987-101 -242-101 -851-101 -681A-76	-09-489-850-20 -09-739-449-1163 -09-839-110-1163 -09-540-236-2245 -09-489-039A-136 -09-489-039A-136 -09-263-681A-792 -10-082-014-12-79 -09-252-691-9162
16 11 11 11 11 7,	e 7451, A 7, Appli 7, Appli e 7, Appl e 3, Appl e 3, Appl e 3, Appl 2, Appli 2, Appli 2, Appli	e 13821, e 13821, e 2792, e 4082, e 4085, f 13845, e 13845,	9162, 123, 1 47, Ap 10149, 10149, 10149, 7684, 19759,	20, 1 11638 11638 2245, 13699 7922, 124, 124, 48, 1

ALIGNMENTS

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US-08-406-362-2

Sequence 2, Application US/08406362

Sequence 2, Application US/08406362

Sequence 2, Application US/08406362

GENERAL INFORMATION: Bernard R
APPLICANT: Brodeur, Bernard R
APPLICANT: Hamel, Josee

ITITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Flop
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TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000

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                                                                                                                                                   US-08-479-520-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09870759
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
                                                                                                       Sequence 20, Application US/08479520 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $OFTWARE: PatentIn version 3.1 SEQ ID NO 36 LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-01
NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
  APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESEI
TITLE OF INVENTION: BACTERIAL AND VII
TITLE OF INVENTION: CNS CARRIER, ANT
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                          121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-596-900
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                            61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%; Score 868; DB 8; Local Similarity 100.0%; Pred. No. 3.9e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                     VAN ALSTYNE, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-05-30
PEPTIDES RÉPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING ACCUS CARRIER, ANTIBODIES THERETO, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 868; DB 22;
100.0%; Pred. No. 3.9e-91;
tive 0; Mismatches 0;
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    AND USES
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                        AGENTS AND THEIR
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                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08486050 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  APPLICANT: VAN ALSTINE, LAWTENCE RAJEDDIRA APPLICANT: SHARMA, LAWTENCE RAJEDDIRA TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING ACTITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 1- 904136
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 07-JU
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                                                         COUNTRY: USA
ZIP: 20007-5109
                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/127,499
                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ATLIALALPAAALAEGASGFYVQADAAH------AKASSSLGS-----AKG 45
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                                                                                                                Washington
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                                                                                              D.C.
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3000 K Street, N.W., Suite 500
                                                                                                                                  3000 K Street, N.W
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                                                                                                                                    N.W., Suite
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TELEPAX: (202)672-5399
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, LAWTENCE RAJENDRA
TITLE OF INVENTION: PEPTIDES REPRESEN
TITLE OF INVENTION: BACTERIAL AND VII
TITLE OF INVENTION: CNS CARRIER, ANTI
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
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                                                                                                           CLASSIFICATION:
                                                                                                                             APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/486,050 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ATLIALALPAAALAEGASGYYQADAAH------AKASSSLGS-----AKG 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
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                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                               D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%; Score 135; DB 8; Length 170; 26.3%; Pred. No. 1.1e-06;
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                                                                                                                                                 US/08/486,050A
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RESULT 6
US-08-988-444-20
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                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 5191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rei
CURRENT APPLICATION DATA
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                                        TELEFAX: 1.36
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TELEFAX: \-
904136
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/988,444 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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3000 K Street, N.W., Suite 500
170 amino acids
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                                                                (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                  US 08/127,499
                                                                                                                                                                                                                                  US 08/486,050
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                                                                                                                 51916/103/INBI
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                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amin
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                                   Query Match
 Matches
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APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                        NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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 41;
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                                                                                                                                                     170 amino acids
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 Conservative
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                                                                                               unknown
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NUMBER: US 08/127,499
28-SEP-1993
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26.3%;
                 15.6%; Score 135; DB 16; 26.3%; Pred. No. 1.1e-06;
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 20; Mismatches
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Pred. No. 1.1e-06;
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 47;
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                                   Length 170;
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                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-489-850-20
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                                                                                                                                                                                  Matches
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                         46 FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                      15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                                        Local Similarity
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                                                                                                                                    6 ATLIALALPAAALAEGASGFYVQADAAH------AKASSSLGS------AKG 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 51916/103/INBITELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-Jan-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 170 amino acids
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                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                        15.6%; Score 135; DB 18; 26.3%; Pred. No. 1.1e-06;
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                                      -----KAPSTDFK 79
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                                                ; ORGANISM: Agrobacterium tumefaciens US-09-803-110-11638
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences
FILE REFERENCE: 38-10(15490)C
CURRENT PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 11638
LENGTH: 281
                                                                                                                                    NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 11638
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11638, Application US/09803110 GENERAL INFORMATION:
    Query Match
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                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/803,110 CURRENT FILING DATE: 2001-03-12 PRIOR APPLICATION NUMBER: US 09/739,449 PRIOR FILING DATE: 2000-12-19 PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)D
                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/168,139 PRIOR FILING DATE: 1999-12-01
                                                                                             TYPE: PRT
                                                                                                                  ENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 V-----KNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 KLRNTSCSVNGLGCDPTTEHGGKGKWRFAYALMAGASIDVTCNLKADIGYRFRHINKGDM 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 SFSQTSI---GLG---------VLTGVSYAVTPNVDLDAGYRYNYIGKVNT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 FAYENGGGPGRDKGLYSHEVRVGGRYVF 259
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Pred. No. 9.8e-06;
  Score 129.5;
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Length 281;
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Query Match
Best Local Similarity
Watches 51; Conserva
                                                                                                     ; SEQ ID NO 13699
; LENCTH: 187
; TYPE: PRT
; ORCANISM: Klebsiella pneumoniae
US-09-489-039A-13699
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                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
LENGTH: 98
TYPE: PRT
ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2245, Application US/09540236 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS ETLE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR EILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIG---KVNTVKNVRSGE--LSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 V------KNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 KLRNTSCSVNGLGCDPTTEHGGKGKWRFAYALMAGASIDVTCNLKADIGYRFRHINKGDM 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 FAYENGGGPGRDKGLYSHEVRVGGRYVF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CGSVPGRCVSADLSSLSAYTLMANAYVDLGTYGSITPYVGG-----GIGGSYVKWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ETKVGFGVLAGAQYAINPQLSVDAGVEYNYLGKYDKLDTASKLKAHQYGAKVGLRHNF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 AAHAKASSSLGSAKGFSPRI------SAGYRINDL---RFAVDYTRYKNYKAPSTDF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKNALAGFLAVLLTGTSAIAADLYQAEPAPAYVDAPEVTVTQASGWYLRGDVGYSFNKLR 60
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                                                                                                                                                                                                                                                                                                                                                                                Gary Breton et. al
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                   Conservative
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               12.6%; Score 109.5; DB 18; 25.2%; Pred. No. 0.0011; % mismatches 78;
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                                                           DB 18;
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US-09-543-681A-7922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7922, Application US/09543681A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Sequence 124, Application US/10082014 GENERAL INFORMATION:
              SOFTWARE: PatentIn version 3.1
SEQ ID NO 124
LENGTH: 21
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                                                                                                        TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY FILE REFERENCE: ICC-130.0 4564/85124 CURRENT APPLICATION NUMBER: 05/10/082,014 CURRENT FILING DATE: 2002-02-22 PRIOR APPLICATION NUMBER: 09/930,915 PRIOR FILING DATE: 2001-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
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                                                                                     NUMBER OF SEQ ID NOS: 290
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TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 MKK---TAIALAVAVAAFATAAQAAPKDNTWYTGGKLGWSQYQSTGNNWDGVNIGNGSTH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDQIGAGAFAGYQYNQYLGFELGYDWLGRMAYKGSYNNGAFKAQGIQLTTKLSYPVMDDL 139
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Search completed: October 28, 2002, 16:11:21
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US-60-358-618-48
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APPLICANT: Birkett, Ashley J.

TITLE OF INVENTION: STABILIZED HBc CHIMER PARTICLES HAVING MENINGOCCOCAL IMMUNOGEN

FILE REFERENCE: ICC107 (4564/82044)

CURRENT APPLICATION NUMBER: U5/60/358,618

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 154

SOFTWARE: Patentin version 3.1

SEQ ID NO 48

LENGTH: 21

TYPE: PRT
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                                                                                                                         Query Match
Best Local Similarity
Matches 21; Conserv
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time : 106.601 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 GKVNTVKNVRSGELSVGVRVK 173
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                                                                                                                                        Score 101; DB 26;
Pred. No. 0.00038;
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Listing first 45 summaries
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J US-09-684-883-6

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	346,		Sequence 350, App	Sequence 53, Appl		Sequence 3443, Ap	Sequence 1, Appli	Sequence 6145, Ap	Sequence 54, Appl	Sequence 4, Appli	Sequence 18, Appl				153,		Sequence 7957, Ap	Sequence 67259, A	Sequence 8424, Ap	Sequence 24508, A	Sequence 5271, Ap	Sequence 47, Appl	Sequence 47, Appl		Sequence 118678,

RESULT 1 US-09-684-883-2 US-09-684-883-2 ISEQUENCE 2, Application US/09684883 GENERAL INFORMATION: APPLICANT: Brodeur, Bernard R Martin, Denis Hamel, Josee Rioux, Clement TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS CORRESPONDENCE ADDRESS: ARDDRESSE: FOley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington CITY: Washington COUNTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION NUMBER: US/09/684,883 FILING DATE: 06-Oct-2000 PRIOR APPLICATION DATA:

TELEX: 904136 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 2

APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-NAR-1995 APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-684-883-2
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US-09-684-883-6
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US-09-684-883-6
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INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
APPLICATION HINDRAMITON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                   NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE_DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brodeur, Bernard R
                  SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
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                                                                             TYPE: amino acid
                                                                                                                                                                           TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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No. 7.4e-83;
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US-09-684-883-30
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Best Local Similarity
Matches 171; Conserv
                 Query Match
Best Local Similarity
  Matches 170; Conservative
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INFORMATION FOR SEQ ID NO: 30:
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                                                                                                                                                                                                                                                                                                    NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,7
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
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                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995 APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                      LENGTH: 175 amino acids
                                                                                                                                                                                                                                                                                     TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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Rioux, Clement
                   96.6%;
97.1%;
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Pred. No. 2.2e-81;
0; Mismatches 3
  0; Mismatches
                       Score 838.5;
Pred. No. 9.:
                                                                                                                                                                                                                                                                                                                                                                  29,768
                                                                                                                                                                                                                                                                                                                                                   047998/0128
                       9.2e-80;
                                        DB 9;
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Indels
                                        Length 175;
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US-09-684-883-8
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Best Local (
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                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDEDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     Match 95.0%;
Local Similarity 94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAVDYTRYKNYKXAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
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                                                                               1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
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                                                        MKKALAALTALALPAAALAEGASGEYVQADAAHAKASSSLGSAKGESPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brodeur, Bernard R
                                                                                                                                        164;
                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/684,883
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                                                                                                                                      Conservative
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Rioux, Clement
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                                                                                                                                                  Score 825; DB 9;
Pred. No. 2.4e-78;
                                                                                                                                      Mismatches
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                                                                                                                                                                     Length 174;
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                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
      121
                    120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTYKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSFVKPYLGARLSLNRASVDLGGSDS 119
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                                                                                                                                                      1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                        1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                          FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                        167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 175 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                      Conservative
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Rioux, Clement
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                                                                                                                                                                                                                                                     95.0%;
95.4%;
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                                                                                                                                                                                                                                  Score 824.5; DB 9; Length 175;
Pred. No. 2.7e-78;
0; Mismatches 7; Indels 1
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                                                                                                                           Sequence 9, Application US/10203942 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                      Matches
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TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
                                         APPLICANT: DENOEL, PHILIPPE APPLICANT: POOLMAN, JAN APPLICANT: THONNARD, JOELLE
                                                                                  APPLICANT: BERTHET, FRANCOIS-XAVIER APPLICANT: DENOEL, PHILIPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                           61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                                                                                                           Local
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)572-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                 FAVDYTRYKNYKAPSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: 608B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/684,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                      Conservative
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                           15.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                           Score 133; pred. No.
                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                           6.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-203-942-9
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SEQ ID NO 45753
LENGTH: 187
TYPE: PRT
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Best Local :
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CURRENT FILLING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT FILE REFERENCE: 38-10(52726)C
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APPLICANT: Edgerton, M
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                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LTRVGKYRPQDKPNTALNYNPWIGSINAGISYRF 214
131 -----SASTSTSLDSVSASA----DTGS-----LAATTSVSAAGAAVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 -----RYNYIGKVNTVKNVRS--GELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DYYGKAGVALVRSDYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLEYQW 180
                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YGYFGGYQILNQNNLGLAVELGYDDFGRAKGREKGKTVVKHTNHGTHLSLKGSYEVLEGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 PRISAGYRI----NDLRFAV-----DYTRYKNYKAPSTDFKLYSIGA--SAIYDFDTQSPV 97
                                          64 DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQT 123
                                                                                       82 AAASLVSAAISGSAASTGAAAASVSAAGAAASGSASLGSASVGSASATA----- 130
                                                                                                                                4 ALATLIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLRFAV 63
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Hinkle, Gregory J.
Kovalic, David K.
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                                                                                                                                                                                                  10.3%; Score 89; DB 11
29.2%; Pred. No. 0.35;
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US-09-791-537-117254
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US-10-219-999-59699
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                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
SEQ ID NO 117254
LENGTH: 576
TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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SEQ ID NO 59699
LENGTH: 229
                                                                                                                 Query Match
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117254, Application US/09791537
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDAN SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
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PRIOR FILING DATE: 2001-99-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 SIGLGVLTGVSYAV-TP 139
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19 AEGASGYYVQADA------AHAKASSSLGS-AKGFSPRISA-GYRINDLRFAVDYTR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQT 123
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                                                                                          Local Similarity
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Hinkle, Gregory J.
Kovalic, David K.
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                                                                      Conservative
                                                                                      10.2%; Score 88.5; DB 9; Length 576; 24.6%; Pred. No. 1.7;
                                                                 29; Mismatches
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 22674
LENGTH: 765
TYPE: PRT
ORGANISM: Synechocystis sp
US-09-791-537-22674
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GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Martin, Denis

Tosee
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APPLICANT: Bionomix, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 FEPYI--GARLINLSFALDQT--TNYRYNSSLVSL--AGQFQINETASRTWINPLVGGKL 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 FSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 10.2%; Score 88.5; Di Local Similarity 26.1%; Pred. No. 2.5; Pes 29; Conservative 20; Mismatches
                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHCIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKNYKAPSTDFKLYSIGASAIYDFDTQSPV----KPYLGARLSLNRASVDLGGSDSFSQT 123
APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                            STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Debe, Derek
                                                                                                                                                                                                                                                                                                                                                                       Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                  RESULT 14
US-10-219-220-149
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US-09-990-004A-149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 204
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 149
LENCTH: 500
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149, Application US/09990004A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
  Sequence
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/990,004A CURRENT FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US 09/327,373 PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lasham, Annette TITLE OF INVENTION: Methods for Modulating Celluar Development and Programmed Cell FILE REFERENCE: 11000.1038c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Flinn, Barry APPLICANT: Lasham, Anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                              151
                                                                                                                                     108 NRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AYNALGEKEKRFQVFKDNLRFIDDHNAGGD-RTYTVGLNQFADLTNEEYRSMYLGARMDR 150
                                                                                                                                                                                                                                                        32 AAVAVLALALALTTIASALDMSIVSYDRAHGDRSSSSSSSWRSDDEVMAVYESWLAKHGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                            4 ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRI------ 56
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                -----NDLRFAY--DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSL 107
                                                                                              SGRRLGRARSD-
149, Application US/10219220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                   41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/406,362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%;
                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 87; DB 9; Length 500 23.7%; Pred. No. 2.1;
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Pred. No.
                                                                                                ---RYAVAAGEELPASVDWRKEGAVVDVKD 188
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. 0.023;
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112202
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Brucella canis
US-09-791-537-112202
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US-09-791-537-112202
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Best Local Similarity
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION UNMBER: U.S. NO. 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 SGRRLGRARSD-------RYAVAAGEELPASVDWRKEGAVVDVKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 NRASYDLGGSDSFSQTSIGLGYLTGYSYAYTPNYDLDAGYRYNYIGKYNTYKN 160
171 RVKF 174
                                                 150 DGESKFRVGWTAGAGLEAKLTDNILGRVEYRYTQYSNKNYDLAGTTVRNKLDTQDIRVGI 209
                                                                                            118 DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRY-----NYIGKVNTVKN-VRSGELSVGV 170
                                                                                                                                                   100 SWAKKSKDGLEVKQGFE-GSLRARVGYDL---NPVMPYLTAGIAGSQIKLN-----NGL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 AYNALGEKEKRFQVFKDNLRFIDDHNAGGD-RTYTVGLNQFADLTNEEYRSMYLGARMDR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 10.0%; Score 87; DB Local Similarity 23.7%; Pred. No. 2.1;
                                                                                                                                                                                                                                                  41 PQYSWAGGYTGLYLGYGWNKAK-TSTVGSIKPDDWKAGAFAGWNFQKDQIVYGVEGDAGY 99
                                                                                                                                                                                                                                                                                              14 PAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISA----GYRINDLRFAVDYTRYK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRI----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NDLRFAV--DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSL 107
                                                                                                                                                                                               NYKAPSTD-----FKLYSIGASAIYDFDTQSPVKPYL----GARLSLNRASVDLGGS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                     9.9%; Score 86; DB 9; Length 213, 25.5%; Pred. No. 0.85; 27. Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  34; Gaps
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Db 210 GYKF 213

Search completed: October 28, 2002, 16:13:49 Job time: 36.6987 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                    ĕo.
                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               824.5
824.5
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                                                                                                                                                                                                                 Score
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length: 2000000000
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874
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                                                                                                                                                                                                                                                                                                                                                                                                                           : //cgn2_6/ptodata/1/paa/US06_COMB.pep: *
    //cgn2_6/ptodata/1/paa/US06_COMB.pep: *
    //cgn2_6/ptodata/1/paa/US06_COMB.pep: *
    //cgn2_6/ptodata/1/paa/US08_COMB.pep: *
    //cgn2_6/ptodata/1/paa/US081_COMB.pep: *
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                                                                                                                                                                                                              Length
       8 US-08-406-362-2
22 US-09-870-759-36
8 US-08-479-520-20
8 US-08-486-050-20
8 US-08-486-050A-20
13 US-08-988-444-20
16 US-09-217-849-20
                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                        SUMMARIES
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(without alignments)
591.158 Million cell updates/sec
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Sequence 2, Appli
Sequence 36, Appl
Sequence 20, Appl
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10.3	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	•	10.7	•	•		•		•	٠		11.3	11.4	11.4	11.4	•	•	•	•	•	٠		٠	٠		•
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US-09-418-980-4 US-09-506-078-44	-60-120-454-4	-809-665A-15	-09-545-199D	-09-545-199C-15	-09-506-078-4	-09-418-980-1	-09-451-184-	-722-	-08-457-997	-08-457-997	8-065-442	09-252-9	80-025-3	-10-015-127	08-331-393-5	-10-072-851-	-09-815-242-10	-US02-03987-10	-09-543-681A-7	-60-358-618-4	-10-082-014-124	-09-328-352-514	-10-072-851-1384	-09-815-242-138	-US02-03987-1384	-60-358-618-	-082-014-123	-252-691C-91	8-09-252-691-916	-09-328-352-533	-09-543-681A-76	-09-540-236-2245	A-136	-09-803-110-	-09-739-449-1163	-09-489-8
e 44, A	46,	e 153,	e 153	e 153,	e 46,	equence 10	ce 2,	e 2,	2,	N	quence 2, Appli	equence 30094,	(D)	e 11706,	quence 5, Appli	e 10149	Sequence 10149,	quence 10149	equence 7922	equence 48,	equence	equence 5146	equence 1384	Sequence 13845,	quence 13845	equence 47,	e 123,	e 9162	equence 9162	equence 5331	e 7684	e 2245	equence 1369	Œ	nce 1163	Sequence 20, Appl

ALIGNMENTS

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US-08-406-362-2
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GENERAL INFORMATION:
APPLICANT: Brodeur, Berna
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, JOSee
            APPLICATION NUMBER: US/08/406,362
FILLING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                STREET: 1251 AV
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                       ZIP: 10020
                                                                                                                                                                                                                                                                                                                        COUNTRY:
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                            1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                        United States of America
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Pharma-43
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TELECOMMUNICATION INFORMATION:

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                                                                                                                                US-08-479-520-20
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SEQUENCE CHARACTERISTICS:
LENGTH: 174 amin
                                                    Sequence 20, Application US/08479520
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSE
FILE REFERENCE: 870759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                                                                                                                         61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
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                                                                                                                                                                                                                                                                                                                         61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
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                                                                                                                                                                                                              FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                             167;
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Similarity 95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%;
                  PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
    CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                               ; Sequence 20, Application US/08486050
; GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                 APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING ACTIVALE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/127,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 01
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin ReloCURRENT APPLICATION DATA:
                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                      135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
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                                                                                                STATE:
                                                                                                                CITY: Washington
                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 114
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TELEX: 90413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                           ZIP: 20007-5109
                                                                         COUNTRY:
                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.C
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3000 K Street, N.W., Suite 500
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                                                                                                                                       3000 K Street, N.W., Suite 500
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 138.5; DB 26.9%; Pred. No. 1e-06;
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, LAWTENCE Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
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                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                    CLASSIFICATION:
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3000 K Street, N.W., Suite 500
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                                                              US 08/127,499
                                                                                                                                        US/08/486,050A
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US-08-988-444-20; Sequence 20, Application US/08988444; GENERAL INFORMATION:
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-- Tocal Similarity
                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
FILING DATE: 08-SEP-1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/:
TELECOMMUNICATION INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
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REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rejendra
TITLE OF INVENTION: PEPTIDES REPRESEN
TITLE OF INVENTION: BACTERIAL AND VIF
TITLE OF INVENTION: CNS CARRIER, ANTI
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/988,444
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                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                    TELEPHONE:
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                                                                                   (202)672-5399
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                                                                                                                             29,768
ER: 51916/103/INBI
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; TOPOLOGY: US-09-217-849-20
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US-09-217-849-20
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Query Match 15.8%; Score 138.5; DB 16; Length 170; Best Local Similarity 26.9%; Pred. No. 1e-06; Matches 42; Conservative 19; Mismatches 48; Indels 47;
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Best Local :
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                                                                                                                                                                                                          TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 5191

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VAN ALSTYNE, DIEGO APPLICANT: SHARMA, LAWTENCE REJENDIA APPLICANT: SHARMA, LAWTENCE REJENDIA THE PRITOPIC SITES FOR TITLE OF INVENTION: BECTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF TITLE OF SEQUENCES: 75
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                        TYPE:
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                                                                                                                                               amino acid
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                          unknown
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28-SEP-1993
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                                                                                                                                                                                                                                                                                                                   51916/103/INBI
47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Gaps
Gaps
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	45 74		-AKASSSLGS- : :: GANNTSTVSDY:	THDYPQATGANN	NDAAH : NDLAYAAERI	EGASGFYVQ <i>I</i> : : DRRSPYYVQ <i>I</i>	AALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKG :: :	20 00	Оy
	ıps 4;	170; 47; Gaps	Length Indels	1e-06; ches 48;	Score 138.5; DB pred. No. 1e-06; 19; Mismatches	15.8%; ilarity 26.9%; Conservative 19	Sim 2;	Query Match Best Local Matches 4	35 M 10
				20:	NO:	ON: ON:	STRANDENDESS: <u STRANDENDESS: <u TOPOLOGY: unknow SEQUENCE DESCRIPTION: 489-850-20</u </u 	09-	vs-
					cids	ID NO: 20: TERISTICS: 0 amino ac	INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 170 amino acids	INFORMAT	
					ATION: -5300 399	ON INFORM (202)672 202)672-5	TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEFAX: (202)672-5399 TELEY AVAI 36	TEI	
				8 1916/103/INBI	A. : 29,768 MBER: 5191	ON NUMBER	NAME: BENT, Stephen A. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:		
				7,499	US 08/127,499 -1993 DN:	N NUMBER: US E: 28-SEP-199 INFORMATION:	APPLICATION NUMBER: US FILING DATE: 28-SEP-19 ATTORNEY/AGENT INFORMATION:	ATT	·· ··
				14	08/988,44 vn>	ON DATA: N NUMBER: E: <unkno< td=""><td>APPLICATION NUMBER: 08/988,444 FILING DATE: <unknown></unknown></td><td>יד א</td><td>., ., .,</td></unkno<>	APPLICATION NUMBER: 08/988,444 FILING DATE: <unknown></unknown>	יד א	., ., .,
				, 000	-2000 known>	E: 24-Jan	FILING DATE: 24-Jan-2000 CLASSIFICATION: <unknown></unknown>		
			# - U C	41.0/ VCTSTOII	: : : : : : : : : : : : : : : : : : :	TION DATA	CURRENT APPLICATION	Cui	
					mpatible °C-DOS/MS-[SYSTEM: P	COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1 0		
					disk	READABLE FORM:	COMPUTER READABLE MEDIUM TYPE:	CO	
						USA 07-5109	7 RY:		. ~. ~.
				Suite 500	et, N.W.,	0 K Stre	STREET: 30		· · ·
							CORRESPONDENCE ADDRESS: ADDRESSEE: Foley &	CO	
THEIR	AGENTS AND ES THEREOF	CAUSING AGE		SE	ERIAL AND	BACT			
				ira	NE, Diane Lawrence Rajendra	VAN ALSTYNE, Diane SHARMA, Lawrence Rajendra VENTION: PERTIDES REPRESE	APPLICANT: VAN ALSTY SHARMA, I TITLE OF INVENTION:	ΤŢ	
					89850	lon US/094	RESULT 8 US-09-489-850-20 ; Sequence 20, Application US/09489850 ; GENERAL INFORMATION:	SULT 8 5-09-489-8 Sequence GENERAL	RES US:
				RASVD 114 : RHSID 170	ARLSLNR :: ARVAYGHVRI	POSPVKPYLGARLS : : :: KGKFKPYIGARVA	LYSIGASAIYDEDTOSPYKPYLGARLSENRASVD : : -	81 L 135 A	Db Qy
	134	QENGTFHA	KKDLKTEN	VNTKELENKHNN	RKWNNNKYS	VRIAADYASY	IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA	75 I	ర్జ
	80	KQVPSTDFK		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	KNY	RFAVDYTRYK	FSPRISAGYRINDLRFAVDYTRYKNY	46 F	Qу
	45 74		-AKASSSLGS : :: GANNTSTVSDYF	TTHDYPQATGAN	ADAAH : ADLAYAAER:	EGASGE I VQAD : : EDRRSPYYVQAD	SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS	15 S	94 63
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                                         ; ORGANISM: Agrobacterium tumefaciens US-09-803-110-11638
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                                                                                                 SEQ ID NO 11638
TENGTH: 281
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LENGTH: 281
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  Query Match
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)D
CURRENT APPLICATION NUMBER: US/09/803,110
CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/739,449
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: US 60/168,139
PRIOR FILING DATE: 1999-12-01
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                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                    TYPE: PRT
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  14.6%;
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  Score 128;
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RESULT 12
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13699
FILING DATE: 1999-01-29
                                                                                       Sequence 2245, Application US/09540236 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709 2004001
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
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                                                                                                                                                                                                                           AGKDGNRDNTLADGAYAGVNFRF 187
                                                                                                                                                                                                                                                                     IGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                 AGGGAELPLGQYFTLF-GEGYYSPDSMSSGVEDYVEANAGVRLNVRPSLNIEAGYRYIDM 164
                                                                                                                                                                                                                                                                                                                                                                                                         DGDSVGLGMGYNFNLGPF - - -
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8; Mismatches 89
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CURRENT APPLICATION

NUMBER:

US/09/540,236

CA

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; ORGANISM: Acinetobacter baumannii US-09-328-352-5331
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US-09-328-352-5331
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; ORGANISM: M.catarrhalis
US-09-540-236-2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-543-681A-7684
                                                                                                                                                                                        Sequence 5331, Application US/09328352
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CUGRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                       NUMBER OF SEQ ID NOS:
SEQ ID NO 5331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 7684
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   Matches
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                                       Query Match
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CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR EILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GARY BRETON
                                                                                                                 LENGTH: 487
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 QTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIG---KVNTVKNVRSGELSA--GVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                         126 GQMEVALNNFS--YNGKEN-QQSKSAFAYGAGIQFNPYPNIAIDASYEYTKLDAFKVGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 --- RLSLNRASVDFNGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIG--KVNT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 EFDNQWGMIGSFVYTHQGYDYHWNSRKIGSIDLDYYSLAAGPVYRFNDYISAYGLVGVAH 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 N-DLRFAV------DYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGA-- 104
                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKLLVPLIMTSLSLCAANAQAVGENTLSLGYAQSHAKVDGDKLKEKPKGFNVK----YRY 65
 l Similarity 29.: 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
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39.7%;
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11.9%; Score 104; DB 17; 29.2%; Pred. No. 0.035; Eive 24; Mismatches 61;
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Pred. No. 0.00022;
Pred. No. 18;
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                                     Length 487;
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Search completed: October 28, Job time: 105.197 secs
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CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 9162
LENGTH: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9162, Application US/09252691B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                           182 YMDIDTDVRFKAGGQQQSINTRLDPWVFMFSAGYR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 DFNGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAG--YRYNYIGKVNTVKNV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                        122 VRPYIGAGVNYTTFFDEKFNDTGKEAGLSDLSLKDSWGMAGQVGLDYLINRDWLINASVW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 LYNGYDADIKETTGAGWLAGAAYQI-PEIALRASVTYRSEIDHKVDINENL
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                                                                                                                                                                                                 98
                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                          59 ---- LRFAVDYTRYKNYKQVPSTDFKLYSIGASAIYDF--
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 RINDLRFAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSL-NRASV 113
                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                          1 MKK-ALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRIND-
                                                                                                              -VDLDAGYRYNYIGK---VNTVKNVRSGELSAGVR 172
                                                                                                                                                                                             VKPYLGARLS-----LNRASVDFNGSDSFSQTSTGLGVLAGVSYAVTPN------
                                                                                                                                                                                                                                     TQLGLTFTYMATDNVGVELLAATPFR-HRVGLGPTGDIATVHHLPPTLMAQWYFGDSSSK 121
                                                                                                                                                                                                                                                                                                                  MKKLAVAALILSSLSGGAYAHEAGEFFIRAGSATVRPTEGSDNVLGM-----GGFNVSNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKATEALQAQGLPVNDQTLALAKGQVLASPQFKQLAGALAAANNYLGNG-GTKVKVDT--
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                                                                                                                                                                                                                                                                                                                                                                                                   48;
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
VENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                  2002, 16:11:22
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 217;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                 US-09-684-883-4
874
1 MKKALAALIALALPAAALAE......VNTVKNVRSGELSAGVRVKF 175
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1465.185 Million cell updates/sec
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: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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sequence sao, App	200,	5000000 000 and		Sequence 350. App	-	Sequence 53, Appl	Sequence 7077, Ap	Sequence 7041, Ap	Sequence 112202,	Sequence 59699, A	Sequence 149, App	sequence 149, App	down your age	~	10 9	Sequence 26, Appl	Sequence 8, Appli-	Sequence 2, Appli	Sequence 6, Appli	Sequence 30, Appl	sequence 4, Appli	- ;	Description	

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US-09-513-996A-58289	US-09-513-996A-13641	US-09-513-996A-67258	US-09-513-996A-58290	US-09-513-996A-13642	US-09-684-883-18	US-60-360-039-22147	US-09-791-537-108323	US-09-791-537-118678	US-09-791-537-89799	US-09-513-996A-64105	US-09-513-996A-64106	PCT-US02-12532-123	US-10-108-605-61	US-09-684-883-23	US-10-053-853A-1674	US-09-791-537-67314	US-10-219-999-45753	US-09-791-537-99401	US-09-791-537-99400	US-09-791-537-58668	US-10-179-131-9383	US-09-791-537-52271	US-10-206-576-106	US-09-791-537-119822
	13641.	67258	Sequence 58290, A	Sequence 13642, A	Sequence 18, Appl	Sequence 22147, A			Sequence 89799, A	Sequence 64105, A	64106	Sequence 123, App	Sequence 61, Appl	Sequence 23, Appl	Sequence 1674, Ap	Sequence 67314, A	ω.	•	Sequence 99400. A		Sequence 9383. Ap		Sequence 106, App	Sequence 119822.

ALIGNMENTS

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MESULT 1

US-09-684-883-4

Sequence 4, Application US/09684883

Sequence 4, Application US/09684883

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Hamel, JOSEE

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/684,883
FILING DATE: 13-MOV-1997
APPLICATION NUMBER: US/08/913,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION NUMBER: 0201672-5399
TELECOMMUNICATION NUMBER: 030498/0128
TELECOMMUNICATION NUMBER: 047998/0128
TELECOMMUNICATION NUMBER: 030498/0128
TELECOMMUNICATION NUMBER: 047998/0128
TELECOMMUNICATION NUMBER: 050/001,983
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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US-09-684-883-30
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GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
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                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
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                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOY-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                              SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                    LENGTH: 175 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                STRANDEDNESS: <Unknown>
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Rioux, Clement
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    30:
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US-09-684-883-6
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                                                                           ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-684-883-6
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Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/684,883 FILING DATE: 06-Oct-2000 PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995 APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                        TELEFAX: (202)672-5399
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Conservative
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Rioux, Clement
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  95.9%; Score 838.5; DB 9
97.1%; Pred. No. 4.9e-80;
tive 0; Mismatches 4
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Pred. No. 1.7e-80;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
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61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
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                                                                                1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION UNMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-NOG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                            MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brodeur, Bernard R
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                                                                                                                                                 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      LENGTH: 174 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
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ZIP: 20007-5109
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                                                                                                                                               Conservative
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                       (202)672-5399
                                                                                                                                                                 94.38;
                                                                                                                                             0;
                                                                                                                                      Score 824.5; DB 9; Length 174;
Pred. No. 1.5e-78;
0; Mismatches 7; Indels 1
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                                                                                                                                                                                                                                         Matches 164;
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09684883 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
120 FSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                             121
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                                                                                  61
                                                                                                61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                 1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                       Match 93.1%;
Local Similarity 93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,7.
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/684,883 FILING DATE: 06-Oct-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                    ESQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                          FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDS
                                                                                                                                                        MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
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ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Denis
                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                     Score 813.5; DB 9;
Pred. No. 2.1e-77;
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                                                                                                                                                                                                                                                                        Length 174;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-684-883-26
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US-09-684-883-26
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                                                                                                                                                                US-10-203-942-9
                                Sequence 9, Application US/10203942
GENERAL INFORMATION:
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DENOEL, PHILIPPE
APPLICANT: POOLMAN, JAN
APPLICANT: THONNARD, JOELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                  61 FAVDYTRYKNYKQVPSTDFKLYSIGA 86
                                                                                                                                                                                                                                                                                                                                                  Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 047998/0128
TELEPHONE: (202)672-5300
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/684,883
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               FAVDYTRYKNYK-APSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)672-5399
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                               13.6%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                  Score 118.5; DB 9
Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 25;
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                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Actinobacillus pleuropneumoniae US-09-545-199F-153
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 153
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 153, Application US/09545199F GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 54; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lowery E., David
APPLICANT: Fuller E., Troy
APPLICANT: Kennedy J., Michael
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/6227.NCP
CURRENT APPLICATION NUMBER: US/09/545,199F
CURRENT FILING DATE: 2000-04-06
DURGENT FILING DATE: 2000-04-06
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CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
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PRIOR FILING DATE: 2001-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/128,689 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/153,453
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ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 YOWLTRYGKYRPODKPNTALNYNPWIGSINAGISYRF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 Y-----RYNYIGKVNTVKNVRS--GELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LDVYGKAGVALVRS--DYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 PRISAGYRI---NDLRFAV-----DYTRYKNYKQVPSTDFKLYSIGA--SAIYDFDTQSP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 VKPYLGARLSLNRASVDFNGSDSFSQTSTGLG------VLAGVSYAVTPNVDLDAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YGVFGGYQILNQNNLGLAVELGYDDFGRAKG-REKGKTVVKHTNHGTHLSLKGSYEVLEG 119
                                                                                                    54 YRINDLRFAVDYTRYKNYKQVPSTDFKLYSIGASAIYDF------DT 94
95 QSPVKP-----YLGARLSLNRASVDFNGSDSFSQTSTGLGVL-----AGVSYA 137
                                                  59 YGIN--RNSVTYGVFGGYQILNQNNF---GLAAELGYDYYGRVRGNVDEFRTVKHSAHGL 113
                                                                                                                                                    1 MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQASFHDGLRALAREYKVGYHRNSFT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALAALIALPAAALAEGA---SGFYVQADAAHAKASSSLGS-----AKGFS 47
                                                                                                                                                                                                       1 MKKALAALIALAAALAEGA---SGFYVQADAAHAKASSSLGSAK-GFSPRI---SAG 53
                                                                                                                                                                                                                                                            54; Conservative
                                                                                                                                                                                                                                                                                 10.7%; Score 93.5; DB 9; 23.2%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 93.5; DB 11; Length 353; 24.9%; Pred. No. 0.27;
                                                                                                                                                                                                                                                            34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Mismatches
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                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                           Length 369;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                              67;
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; ORGANISM: Eucalyptus grandis US-10-219-220-149
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                                                                                                                                    APPLICANT: Flin, Barry
APPLICANT: Lasham, Annette
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CUGRENT ILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. 09/325,932
PRIOR APPLICATION NUMBER: U.S. No. 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
Query Match
Best Local Similarity 22.1
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Methods for Modulating Celluar Development and Programmed Cell
FILE REFERENCE: 11000.1038c1
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PRIOR APPLICATION NUMBER: US 09/327,373
PRIOR FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 AYNALGEKEKRFQVFKDNLRFIDDHN-----AGGDRTYTVGLNQFADLTNEEYRSM 142
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                                   Score 89.5; D. Pred. No. 1.1;
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Pred. No. 1.1;
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                Indels
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          Gaps
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APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR
FILE REFERENCE: 38-10(52725)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 59699
LENGTH: 229
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US-09-791-537-112202
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US-10-219-999-59699
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Best Local Similarity
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                   APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
TILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
SOFTWARE: PatentIn version 3.0
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; TYPE: PRT
; ORGANISM: Brucella canis
US-09-791-537-112202
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US-09-540-209B-7041
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APPLICANT: GATY L. Breton
APPLICANT: GATY L. Breton
APPLICANT: GATY L. Breton
APPLICANT: GATY L. Breton
AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7077
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APPLICANT: GARY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7041
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TYPE: PRT
ORGANISM: B.fragilis
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                                                                                                                                                                                                                                                                                                   301 QVYGQVNYGKGI 312
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                                                                                                                                                                                                                                                                                                                                                                                                                           92 FDTQSPVKPYLGARLSLNRASVDFNGS-DSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 PRISAGYRINDLRFAVDYTRYKNYK-----QVPSTD-----FKLYSIGASAIYD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 9.9%;
Local Similarity 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNGSAFYRTTQLSYMCD--KLKNWKFGVGVEMPSVDGTTNQYLTINTQRMPDFTASAQYN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDGESKFRYGWTAGAGLEAKLTDNILGRYEYRYTQYSNKNYDLAGTTYRNKLDTQDIRYG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRY-----NYIGKVNTVKN-VRSGELSAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWAKKSKD--GLEVKQGFEGSLRARVGYDL---NPVMPYLTAGIAGSQIKLN-----NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 431;
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US-10-193-002-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/10193002 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 501
TYPE: PRT
ORGANISM: B.fragilis
                                                                       TELEFAX: (206) 682-61
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 TVK-NVRSGEL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 NIEANIGGGEM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 VLPINIFNGTNKYSVDSYMRGKQMIFGLQLGATYRITDYLSAFAGVRMNYVSNGYEGHIR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 -----FNGSDSFSQTS-----TGLGVLAGVSYAVTPNVDLDAGYRYNYI-----GKVN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AV----YKKDKWAFSGNFAVTGGGGKATFNEGLGSFESLVSVVP--GMLVAAGNEMVDKG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AGVAFMENGFHLSLNGQSAFQTRTITST--FAP--FAGFGGNATKVYKGEASAPFIPSVF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 9.9%; Score 86.5; DI Local Similarity 23.6%; Pred. No. 2.3; Mismatches 45; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AVDYTRYKNYKQVPSTDFKLYSIGASAIYD-----FDTQSPVKPYLGARLSLNRASVD-- 114
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAX-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
                                                      SEQUENCE CHARACTERISTICS:
                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                     REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STRANDEDNESS: single
                     TYPE: amino acid
                                   LENGTH: 332 amino acids
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Hendrickson, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-Neto, Antonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEED and BERRY LLP
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                                                                                                 682-6031
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                                                                                                                                                            210121.417C9
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                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
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11: /cgn2_6/ptodata/1/paa/U

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868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : /cgn2_6/ptodata/1/paa/US083_COMB.pep: *
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Result		Query				
No.	Score	Match	1	Ħ	Ħ	Description
_	854	- 1	- 1	œ ¦	US-08-406-362-2	Sequence 2. Appl
N	854	98.4	174	22	US-09-870-759-36	Sequence 36, Apr
ω	135	15.6	170	8	US-08-479-520-20	Sequence 20, Appl
4	135	15.6	170		US-08-486-050-20	Sequence 20, Appl
ហ	135	15.6	170		US-08-486-050A-20	Sequence 20, Appl
σ	135	15.6	170	<u>, ,</u>	US-08-988-444-20	Sequence 20, Apr
7	135	15.6	170	16	US-09-217-849-20	Sequence 20, App

40	4.4	4.5	42	4	40	. u	, <u>u</u>	3 2	6	ω	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8
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10.1	•	•	•	•	•	•	•	10.4	•	•	•	•	•	•	•	•	•	•	•		•	•	٠	•	•	11.2	•	•		٠		٠			15.0		
213	213	178	178	369	369	369	225	643	397	385	568	257	257	257	359									212	212	21	21	21	21	217	217	384	98	187	281	281	170
22	21	22	21	22	19	19	24	17	23				22			80	œ	8	4	16	19	17	24	22	_	26	24	26	24	16	16	19	19	18	22	21	18
US-09-803-110-8555	-09-739-449-855	-09-803-110-937	-09-739-449-937	-09-809-665A-15	545-199D-15	-09-545-199C-15	-10-015-127-138	-09-328-352-5146	902-540-1626	-039A-74	393-5	-851-1384	242-	3987-1384	-184-	'n	US-08-457-997A-2	US-08-457-997-2	442-2	1A-197	7	2-5331	7	-09-815-242-1014	US02-03987-1014	-60-358-6	-10-082-014-	-60-358-618-	-10-082-014-123	09-252-6910	-09~252-691-9162	-09-543-681A-7	-09-540-236-2245	9-039A-136	-09-803-110-1	-09-739-449-1163	-09-489-8
e 8555,	Sequence 8555, Ap	9372,	nce 9372,	equence 153,	Sequence 153, App	equence 153, A	13821,	æ	e 16267,	e 7451,	5, Appli	13845	ര	quence 1	D.	N	N.	N	Appl			5331, A	e 10149.	Sequence 10149,	1014	Sequence 124, App	ر د د	equence 47	123	916	916	equence 792	e 224	e 13699.	e 11638.	e 11638.	Sequence 20, Appl

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US-08-406-362-2
US-08-06-362-2
; Sequence 2, Application US/08406362
; GENERAL INFORMATION:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PROFITCH WATER
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                 ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                             STREET: 1251 AVECITY: New York
STATE: New York
                                                                                          CLASSIFICATION:
                                                                                                                  FILING DATE:
                                                                                                                                   APPLICATION NUMBER: US/08/406,362
                                                                                                                                                                                                                                                                                                                          COUNTRY:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                      10020
                                                                                                                                                                                                                                                                                                                          United States of America
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Pharma-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/09870759 GENERAL INFORMATION:
                                                                                                                        Sequence 20, Application US/08479520 GENERAL INFORMATION:
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Best Local 9
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Best Local :
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CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 870759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TERMAN, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
APPLICANT: VAN ALSTYNE, DIENE RAJENDIA
APPLICANT: SHARMA, LAWTENCE RAJENDIA
APPLICANT: SHARMA, LAWTENCE RAJENDIA
TITLE OF INVENTION: DECTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
THTO OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
THTO OF INVENTION: THE AND THE ANTIBODIES THERETO, AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                     121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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Local Similarity 98.3%;
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                                                                                                                                                                                                                                                  SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%; Score 854; DB 22; 98.3%; Pred. No. 3.9e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MEMINGITIS CAUSING AGENTS AND
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                  US-08-486-050-20
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Best Local Similarity 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 519
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5700
TELEPHONE: (202)672-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/127,499
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ANTORNEY/AGENT INFORMATION:
ANALY: PRIOR OF TABLEY AGENT INFORMATION:
               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
COMPUTER:
                                                                               COUNTRY:
                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                  3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                    USA
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00 K Street, N.W., Suite 500
IBM PC compatible
                                                                                                                                                                      Foley & Lardner
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Pred. No. 1.6e-06;
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                                                                                                                                                Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 170;
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VAN ALSTINE, LANCE RAJENDER REPRESENTING EPITOPIC SITES FOR TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                        SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/486,050A FILLING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
                                     APPLICATION NUMBER: US 0 FILING DATE: 28-SEP-1993
                                                                                                                                                                                                                                                                                                                 STREET: 3000 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                  20007-5109
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3000 K Street, N.W., Suite 500
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Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.6%; Score 135; DB 8; Length 170; 26.3%; Pred. No. 1.6e-06;
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                                                       US 08/127,499
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; GENERAL INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
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TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                           APPLICATION NUMBER: US 08/127,499
FILLING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/10:
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APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESEI
TITLE OF INVENTION: BACTERIAL AND VII
TITLE OF INVENTION: CNS CARRIER, ANT
                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 07-JUN-1
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MEDIUM TYPE: Floppy disk
                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELEFAX: (202)672-5399
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                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                    (202)672-5300
(202)672-5399
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                                                                                                                                                                                                                                                                   07-JUN-1995
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                                                                                                                                                                                                                                                                                      US 08/486,050
                                                                                                                                                                                                                                                                                                                                                                   US/08/988,444
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                                                                                                                                                 51916/103/INBI
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                                                                    US-09-217-849-20
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                                 Query Match
 Matches
                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                     FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/NOCKET NUMBER: 5191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
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                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                 Local Similarity
                                                                                                                                    LENGTH:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                    unknown
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15.6%; Score 135; DB 16; 26.3%; Pred. No. 1.6e-06; tive 20; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                               US/09/217,849
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Pred. No. 1.6e-06;
0; Mismatches 47
                                                                                                                                                                                                                                                          51916/103/INBI
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ropology: unknown sequence description: Seq ID No: US-09-489-850-20
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GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
                                                                                                                                                                               Matches
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 ASSLGLSAIYDFKLKGKFKPYIGARVAYGHVRHSID 170
                                                                                       15
                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                         6 ATLIALALPAAALAEGASGFYVQADAAH------AKASSSLGS------AKG 45
                                                                                                                                6 ATLIALALPAAALAEGASGFYVQADAAH-----AKASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/988,444

FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 08/127,499

FILING DATE: 28-SEP-193

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PEPTIDES RÉPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND
CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                       SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/489,850 FILING DATE: 24-Jan-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A.
                                                                                                                                                                               Conservative
                                                                                                                                                                                                   15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Rajendra
                                                                                                                                                                               20;
                                                                                                                                                                                                   Score 135; DB 18; Pred. No. 1.6e-06;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                           20:
                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                               47;
                                                                                                                                                                                                                        Length 170;
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US-09-739-449-11638, Application US/09739449

Sequence 11638, Application US/09739449

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Ger

FILE REFERENCE: 38-10(15490)C

CURRENT APPLICATION NUMBER: US/09/739,449

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 09/514,000

PRIOR FILING DATE: 2000-02-23

NUMBER OF SEQ ID NOS: 13351

SEQ ID NO 11638

LENGTH: 281
                                         ; ORGANISM: Agrobacterium tumefaciens US-09-803-110-11638
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                                                                                                             PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: US 60/168,139
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 11638
                                                                                                                                                                                                                                                                                                                                                                              Sequence 11638, Application US/09803110 GENERAL INFORMATION:
     Query Match
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/803,110
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/739,449
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
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                                                                                                                                                                                                                                                                                         APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)
                                                                              TYPE: PRT
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                                                                                               ENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 FAYENGGGPGRDKGLYSHEVRVGGRYVF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 KLRNTSCSVNGLGCDPTTEHGGKGKWRFAYALMAGASIDVTCNLKADIGYRFRHINKGDM 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GAHYYQGGPGGYLQDFDTATIKDSYVIGGGVGYQFNNYFRSDVTLDYMGKSDFRGSTSGF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGS----D 118
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 Score 130.5;
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22;
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Length 281;
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TYPE: PRT
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RESULT 12
US-09-540-236-2245
; Sequence 2245, Application US/09540236
; Sequence 2245, Application US/09540236
; GENERAL INFORMATION:
; APPLICANT: GATY L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; FILE REFERENCE: 2709.2005-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-13699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 199-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13699, Appl GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                166 GKDGNRDNTLADGAYAGVNFRF 187
                                                                                                                                                                                                                                                                                                                                                                                                  153 GKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 YLGARLSLNRASVDLGGSDSFSQTSTGLGV-----LAGVSYAVTPNVDLDAGYRY-NYI 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 KLRNTSCSVNGLGCDPTTEHGGKGKWRFAYALMAGASIDVTCNLKADIGYRFRHINKGDM 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 DGDSVGLGMGYNFNLGPF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 MKSIAAKMVAVTIALGASSAACAAVNLHGEAGAEFTNLSASFGAGEPGMTFSSQWAHSDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKALATLIA--LALPAAALAEGASGFYVQADAAHAKASSSLGSAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAELPLGQ-YFTLFGEGYYSPDSMSSGVEDYVEANAGVRLNVRPSLNIEAGYRYIDMA 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIY----DFDTQSPVKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFSQTS---TGLG-------VLAGVSYAVTPNVDLDAGYRYNYIGKVNT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 115.5; DB 18; 26.2%; Pred. No. 0.00031; tive 25; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMTLGGKAVYLNPKDGDEGYAIAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 187;
                                                                                                                                    RELATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .---- 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Proteus mirabilis US-09-543-681A-7922
us-09-252-691-9162
                                                                                                                                                                                                                                                                                                                                 US-09-252-691-9162
                                                                                                                                                                                                                                                        Sequence 9162, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
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NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7922
LENGTH: 384
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                                                                                         SEQ ID NO 9162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-543-681A-7922
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TYPE: PRT
                 TYPE: PRT ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                     ENGTH: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                  198 YQWINNIGDKGTL-NARPDNGMLSVGVAYRF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIG---KVNTVKNVRSGELSA--GVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 YRY-NYIGKVNTVKNVR--SGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 DVYTRLGGMVWRADSTATINATSA--GTQKRFSENDTGVSPVFALGTEYAITPNIATRLE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 SPRIS----AGYRIND---LRFAYDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 KPY--LGARL-----SLNRASVDLGGSDSFSQTSTGLGVL--AGVSYAVTPNVDLDAG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 KDQIGAGAFAGYQYNQYLGFELGYDWLGRMAYKGSYNNGAFKAQGIQLTTKLSYPVMDDL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 MKK---TAIALAVAVAAFATAAQAAPKDNTWYTGGKLGWSQYQSTGNNWDGVNIGNGSTH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKALATLIALALPAAALAEGASG-----FYVQADAAHAKASS-----SLGSAKGF 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 106.5; DB 19; 26.1%; Pred. No. 0.0095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
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US-09-252-691C-9162
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Search completed: October 28,
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PRIOR FILING DATE: 1998-02-18,
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 9162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9162, Application US/09252691C GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691C
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                             178 ASVWYMDIDTDVRFKAGGQQQSINTRLDPWVFMFSAGYR 216
                                                                                                                                                                              118 SSSKVRPYIGAGVNYTTFFDEKFNDTGKEAGLSDLSLKDSWGMAGQVGLDYLINRDWLIN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 ASVWYMDIDTDVRFKAGGQQQSINTRLDPWVFMFSAGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 -----VDLDAGYRYNYIGK---VNTVKNVRSGELSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 SSSKVRPYIGAGVNYTTFFDEKFNDTGKEAGLSDLSLKDSWGMAGQVGLDYLINRDWLIN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 TQSPVKPYLGARLS------LNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPN---- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TQLGLTFT----YMATDNVGVELLAATPFR-HRVGLGPTGDIATVHHLPPTLMAQWYFGD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 LRFAVDYTRYKNYKA------PSTDFKLYSIGASAIYDF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 11.8%; Score 102; DB 1 Local Similarity 22.4%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 MKKLAVAALILSSLSGGAYAHEAGEFFIRAGSATVRPTEGSDNVLGM-----GGFNVSNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKK-ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRI-ND 58
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKK-ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRI-ND 58
                                                                                                                        -----VDLDAGYRYNYIGK---VNTVKNVRSGELSAGVR 171
                                                                                                                                                                                                                                 TQSPVKPYLGARLS------LNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPN----
                                                                                                                                                                                                                                                                                    TQLGLTFT----YMATDNVGVELLAATPFR-HRVGLGPTGDIATVHHLPPTLMAQWYFGD 117
                                                                                                                                                                                                                                                                                                                                                                                  MKKLAVAALILSSLSGGAYAHEAGEFFIRAGSATVRPTEGSDNVLGM-----GGFNVSNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Conservative
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  2002, 16:11:23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76; Indels
                                                                                                                                                                                                                                                                                                                                       -----D 92
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Job time : 104.601 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                  868
854
847.5
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868
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:/cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
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Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-684-883-4
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US-09-684-883-26
US-09-684-883-26
US-09-513-96A-67258
US-09-513-96A-67258
US-09-513-996A-7956
US-09-513-996A-7956
US-09-515-996A-7956
US-09-540-2099-7937-22674
US-09-545-199F-1537
US-09-540-209B-7537
US-09-540-209B-7537
US-09-540-209B-7537
US-09-990-004A-1149
US-10-219-220-1479
US-09-791-537-60560
US-09-791-537-60560
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Sequence 6, Appli
Sequence 2, Appli
Sequence 30, Appli
Sequence 4, Appli
Sequence 26, Appli
Sequence 9, Appli
Sequence 7956, A
Sequence 7956, A
Sequence 22674, A
Sequence 2537, Appli
Sequence 153, Appli
Sequence 153, Appli
Sequence 149, Appli
Sequence 149, Appli
Sequence 149, Appli
Sequence 22903, A
Sequence 2753, Apsli
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US-09-684-883-14	US-09-458-180-2	US-10-179-131-8424	US-10-108-260A-3443	US-10-108-260-3443	US-09-905-176-22	US-09-791-537-119822	US-09-540-209B-6145	PCT-US02-12532-123	US-09-882-227-80	US-09-956-508A-4	US-09-570-214B-7	US-09-684-883-18	US-09-513-996A-64105	US-09-513-996A-64106	US-09-791-537-117254	US-09-540-209B-5271	US-09-791-537-115703	US-09-791-537-80797	US-09-540-209B-7041	US-09-684-883-23	US-09-791-537-112202	US-09-513-996A-39219	US-09-513-996A-7957	US-09-545-199F-151
Sequence 14, Appl	2. Appl		3443	e 3443,		11982		123	80	4.					117254		115703		704		1122(39219		Sequence 151, App

ALIGNMENTS

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US-09-684-883-6
; Sequence 6, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
Martin, Denis
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC-POTATION
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US/08/913,362
FILING DATE: 17-NAR-1995
APPLICATION NUMBER: US 60/001,983
                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                               NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,7 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K St
CITY: Washington
STATE: D.C.
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Rioux, Clement
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US-09-684-883-2
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US-09-684-883-2
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                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION UNMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/684,883 FILING DATE: 06-Oct-2000 PRIOR APPLICATION DATA:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                 TELEX: 904136
                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                          NAME: Bent, Stephen A.
                                                                                                   ENGTH: 174 amino acids
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Rioux, Clement
                                                                                                                                                                                  3: (202)672-5300
(202)672-5399
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RESULT 3
US-09-684-883-30
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                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 30: US-09-684-883-30
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Best Local Similarity
Matches 171; Conserv
   Best Local Similarity Matches 172; Conserv
                                       Query Match
                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-NAR-1995 APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                  TELEX: 904136
                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                              NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                            LENGTH: 175 amino acids
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 Conservative
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Rioux, Clement
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                                                                                                                                                                                                                                                                     (202)672-5399
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                   97.6%;
98.3%;
                                                                                                                                                                                                                                                                                         (202)672-5300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF NEISSERIA MENINGITIDIS
Score 847.5;
Pred. No. 2.1e
0; Mismatches
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Pred. No. 4.4e-80;
                                                                                                                                                                                                                                                                                                                                              29,768
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                       2.1e-79;
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                                       Length 175;
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US-09-684-883-4
; Sequence 4, Application US/09684883
; GENERAL INFORMATION:
GENERAL INFORMATION:
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                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FSQTSXGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                     Match 96.6%; score 838.5; DB 9 Local Similarity 97.1%; Pred. No. 1.8e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
                                                         61 FAVDYTRYKNYKXAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                              1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995 APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                  LENGTH: 175 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                        Conservative
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Martin, Denis
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Rioux, Clement
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                                                                                                                                        Mismatches
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                                                                                                                                                                       DB 9; Length 175;
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; Sequence 8, Application US/09684883
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                Matches 166;
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDEDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                 61
                                                                                                                                                                   1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
APPLICATION NUMBER: US 08/406,362
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brodeur, Bernard
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                                                                          FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bent, Stephen A REGISTRATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/684,883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Rioux, Clement
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                                                                                                                                                                                                                                               96.1%;
95.4%;
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                                                                                                                                                                                                                                         Score 834; DB 9; Length 174; Pred. No. 5.2e-78;
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RESULT 6
US-09-684-883-26
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GENERAL INFORMATION:
APPLICANT: Brod
                                                                                                                                  Sequence 9, Application US/10203942 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Matches
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APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DENOEL, PHILIPPE
APPLICANT: POOLMAN, JAN
APPLICANT: THONMARD, JOELLE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 26:
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APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
APPLICATION NUMBER: US 60/001,983
APPLICATION NUMBER: US 60/001,983
APPLICATION NUMBER: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
ARGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                        61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                  1 FAVDYTRYKNYKAPSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS_MS-DOS
OPERATING SYSTEM: PC-DOS_MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 047998/0128
TELEPHONE: (202)072-5300
TELEPHONE: (202)072-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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LENGTH: 25 amino acids
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Neisseria meningitidis STRAIN: 608B
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                               Score 133; ; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 67258
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67258, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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LENGTH: 353
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Best Local Similarity
                                                                                                                                      Matches
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Best Local Similarity
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CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: ENCODED THEREBY FILE REFERENCE: 2750-709P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: B45210
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                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE LOCATION: 1..339 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                OTHER INFORMATION: Location 1..339 / Ceres Seq. ID 2177695
                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 -----RYNYIGKVNTVKNVRS--GELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LTRVGKYRPQDKPNTALNYNPWIGSINAGISYRF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DVYGKAGVALVRSDYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLEYQW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 KPYLGARLSLNRASYDLGGSDSFSQTSTG-----LGVLA-GVSYAVTPNVDLDAGY-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YGYFGGYQILNQNNLGLAVELGYDDFGRAKGREKGKTYVKHTNHGTHLSLKGSYEVLEGL 120
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  90 DFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGVLA---GVSYAVTPNVDLDAG 146
                                              18 SFSSAKMFIESFKVESPNVK--YTENEIHSVYDYETTEVVHEKTVNGTYQWIVKPKTVKY 75
                                                                                     39 SLGSAKGF-----SPRISAGYRINDLRFAVDY--TRYKNYKAPSTDFKLYSIGASAIY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQASFHDGLRALAREYKVGYHRNSFT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKALATLIALALPAAALAEGA---SGFYVQADAAHAKASSSLGS-----AKGFS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRISAGYRI---NDLRFAV-----DYTRYKNYKAPSTDFKLYSIGA--SAIYDFDTQSPV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                   39;
                                                                                                                                      Conservative
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24.8%;
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                                                                                                                                                        Score 89.5; DB Pred. No. 0.87;
                                                                                                                                        Mismatches
                                                                                                                                                                               DB 9;
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                                                                                                                                        53;
                                                                                                                                                                             Length 339;
                                                                                                                                        Indels
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US-09-791-537-22674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-996A-7956
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
SEQ ID NO 22674
LENCTH: 765
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22674, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7956, Application US/09513996A GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 7956
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCODED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: UNSURE LOCATION: 1..534
OTHER INFORMATION: any n or xaa = unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
106 SLNRASV------DLGGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRY 149
                                                 630 FEPYI--GARLINLSFALDQT--TNYRYNSSLVSL--AGQFQINETASRTWINPLVGGKL 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 YRYNYIGKVNTVKNVRSGELS 167
                                                                                     46 FSPRISAGYRINDLRF&VDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARL 105
                                                                                                                                                     Match 10.3%; Score 89.5; DB 9; Length 765; Local Similarity 26.1%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 SLGSAKGF------SPRISAGYRINDLRFAVDY--TRYKNYKAPSTDFKLYSIGASAIY 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFKTDIRV-PKLGVML-----VGLGGNNGSTLTA---GVIANKEGISWATKDKVQ---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGVLA---GVSYAVTPNVDLDAG 146
                                                                                                                                          29;
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                                                                                                                                        Conservative
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27.7%; Pred. No. 1.
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                                                                                                                                    20; Mismatches
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                                                                                                                                    49;
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                                                                                                                                    Indels 13;
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US-09-545-199F-153; Sequence 153, Applic; GENERAL INFORMATION:
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APPLICANT: Cao, Yongwei
             Matches
                                                Query Match
                                                                                                                                                  SEQ ID NO 153
LENGTH: 369
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LENGTH: 229
                              Best Local Similarity
                                                                                                                                                                                                                                                                                                             APPLICANT: Lowery E., David
APPLICANT: Fuller E., Troy
APPLICANT: Kennedy J., Michael
TITLE OF INVENTION: Anth-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/6227.NCP
CURRENT APPLICATION NUMBER: US/09/545,199F
CURRENT FILING DATE: 2000-04-06
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                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/128,689
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 165
SOFTMARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 63520
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APPLICANT:
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                                                                                                                                     TYPE: PRT
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                                                                                                        ORGANISM: Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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          49;
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Hinkle, Gregory J.
Kovalic, David K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09545199F
        Conservative
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                            21.5%;
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        36;
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                          Score 89;
Pred. No.
        Mismatches
                                             DB 9;
      85;
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                                           Length 369;
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    Indels
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US-09-540-209B-7537
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SEQ ID NO 7537
LENGTH: 165
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APPLICANT: GATY L. Breton
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION UNDEER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09684883 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 DTTDFA-----FGAEAGYAFFLTRTVTIEPAVYYDL-----SEKDSDLSKFGLKVGF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 GSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSA-GVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 YGINRNSVTYGVFGGYQILNQNNFGLAAELGYDYYGRVRGNVDEFRTVKHSAHGLNLALK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 -DFDTQSPVKPYLGARLSLNRASVDLGGSDSFSQTSTGLGVL-----AGVSYAVTPNV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FLYDNVALMLTAGANWSKPEDK---YTLGYGGRYYFD---KCGIYLGAGLKMNRYNWKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FAVD-----YTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                             Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELAARVEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                         ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                  STATE: D.C
                                                                                                                                COUNTRY: USA
                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                               Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.1%; 22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
  Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88; DB 9
Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                              Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ELSAGVRVKF 174
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STRAIN: 608B
SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-09-684-883-15
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US-09-990-004A-149
                                                                                                                                                                                                                                                                                                  ; ORGANISM: Eucalyptus grandis US-09-990-004A-149
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 149, Application US/09990004A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Methods for Modulating Celluar Development and Programmed Cell
FILE REFERENCE: 11000.1038c1
CURRENT APPLICATION NUMBER: US/09/990,004A
CURRENT FILING DATE: 2002-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/327,373 PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
108 NRASYDLGGSDSFSQTSTGLGYLAGYSYAYTPNVDLDAGYRYNYIGKVNTVKN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAVDYTRYKNYKAPST 76
                                          92 AYNALGEKEKRFQVFKDNLRFIDDHNAGGD-RTYTVGLNQFADLTNEEYRSMYLGARM--
                                                                                                                            32 AAVAVLALALATTIASALDMSIVSYDRAHGDRSSSSSSSWRSDDEVMAVYESWLAKHGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                     4 ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRI----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995 APPLICATION NUMBER: US 60/001,983 FILING DATE: 04-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                    -----NDLRFAV--DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16 amino acids
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                     10.0%;
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                                                                                                                                                                                                                                   Score 87; DB 9; Length 500; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 16;
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Db 149 ------DRSGRRLGRARSDRYAVAAGEELPASVDWRKEGAVVDVKD 188

Search completed: October 28, 2002, 16:13:52 Job time: 36.6987 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PC;

2: /cgn2_6/ptodata/1/paa/US;

3: /cgn2_6/ptodata/1/paa/US;

4: /cgn2_6/ptodata/1/paa/US;

6: /cgn2_6/ptodata/1/paa/US;

6: /cgn2_6/ptodata/1/paa/US;

6: /cgn2_6/ptodata/1/paa/US;

9: /cgn2_6/ptodata/1/paa/US;

9: /cgn2_6/ptodata/1/paa/US;

10: /cgn2_6/ptodata/1/paa/U;

11: /cgn2_6/ptodata/1/paa/U;

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13: /cgn2_6/ptodata/1/paa/U;

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17: /cgn2_6/ptodata/1/paa/U;

18: /cgn2_6/ptodata/1/paa/U;

19: /cgn2_6/ptodata/1/paa/U;

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24: /cgn2_6/ptodata/1/paa/U;

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27: /cgn2_6/ptodata/1/paa/U;

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28: /cgn2_6/ptodata/U;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
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870
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'Cgn2_6/ptodata/1/paa/US07_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US081_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US081_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US081_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US084_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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'Cgn2_6/ptodata/1/paa/US089_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US089_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US089_COMB.pep:*
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14d
14d
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4004D0C	Result
825 825 125 125 125 125 125	Score
94.8 94.8 14.4 14.4	% Query Match
174 174 170 170 170 170 170 170	Query Query Match Length DB ID
13 113	80
US-08-406-362-2 2 US-09-870-759-36 US-08-479-520-20 US-08-486-050-20 US-08-486-050A-20 US-08-988-444-20 6 US-09-217-849-20	SUMMARIES ID
Sequence 2, Appl. Sequence 36, App. Sequence 20, App.	Description

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364	364	364	354	364	190	799	397	369	369	369	257	257	257	487	212	212	212	369	369	369	21	21	384	21	21	359	359	359	359	359	217	217	98	187	281	281	170
22	19	2	<u>.</u>	, E	19	16	23	22	19	19	24	22	1	17	24	22	۳,	26	19	18	26	24	19	26	24	18	8	œ	œ	4	16	16	19	18	22	21	18
US-09-809-665A-151	-09-545-	-09-545-199C-15	-09-506-	-09-418-980-8	-09-543-681A	-201-228F	-09-	-09-809-665F	US-09-545-199D-153	US-09-545-199C-153	US-10-072-851-13845	US-09-815-242-13845	PCT-US02-03987-13845	US-09-328-352-5331	US-10-072-851-10149	-09-815-242-10	PCT-US02-03987-10149	US-60-120-454-46	-09-506-078-4	US-09-418-980-10	-60-358-618-4	-10-082-014-12	-09-543	-60-358-	-10-	1	467-722-2	4	457-997-	65-442-2		-09-	-09-540-236-2245	136	-09-803-110-11	-09-739-449-1163	US-09-489-850-20
151,	151,	151,	45		768	203,		153,	153,	153, Ap		Sequence 13845, A	13845,	5331, A		10149	10149	46,	46,	10,	48	124	792	47,	123	ი ა	ν,	2	٧.	2, Appl	9162		2245.	13699,	116	1163	Sequence 20, Appl

ALIGNMENTS

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US-08-406-362-2
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APPLICATION NUMBER: US/08/406,362
ETLING DATE:
CLASSIETCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                          STREET: 1251 Ave
CITY: New York
STATE: New York
COUNTRY: United:
ZIP: 10020
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                                                                                                                                                                                                                                                                               United States of America
Pharma-43
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                                                                                                                                                 US-08-479-520-20
Sequence 20, Application US/08479520
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PAPTIDES REPRESEN
TITLE OF INVENTION: BACTERIAL AND VIR
TITLE OF INVENTION: CNS CARRIER, ANTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/09870759 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/870,759 CURRENT FILING DATE: 2002-01-14 PRIOR APPLICATION NUMBER: US 60/208,128 PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TERMAN, David S TITLE OF INVENTION: COMPOS: FILE REFERENCE: 870759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SKTSAGIGVLAGVSYAVTÞNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
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Local Similarity 94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                                                                                                                                                      SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164;
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      PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING ACCNS CARRIER, ANTIBODIES THERETO, AND USES
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94.3%;
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Pred. No. 9.7e-85;
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          AND USES
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Matches 37; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                 APPLICANT: VAN ALSTYNE, Diane APPLICANT: SHARMA, LAWTENCE RAJENDIA TITLE OF INVENTION: PEPTIDES REPRESEN TITLE OF INVENTION: BACTERIAL AND VIITITLE OF INVENTION: CNS CARRIER, ANTI
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 ASSLGLSAIYDFKLKGKFKPYIGARVA 161
                                                               COUNTRY:
ZIP: 200
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                                                                                                    CITY: Washington STATE: D.C.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               20007-5109
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(202)672-5399
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                                                                                       USA
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                                                                                                                                                                                                                                     CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
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Pred. No. 2.4e-05;
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US-08-486-050A-20; Sequence 20, Application US/08486050A; GENERAL INFORMATION:
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FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 5191
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                APPLICATION NUMBER: US/08/486,050.
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 426-SEP-193
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARKA, LAWTENCE Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
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                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
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BENT, Stephen A.
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                                                                                                                                                                                                                                                                                                                                                       E: Foley & Lardner
3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.4%; Score 125; DB 8; 25.2%; Pred. No. 2.4e-05;
                                                                                                                                      US/08/486,050A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
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              TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
                                                                                                 TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PAPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGE
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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TOPOLOGY: ur
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                                                                                                                                                    29,768
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                                                                                                                                    51916/103/INBI
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                                                                            US-09-217-849-20
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Matches
                                   Query Match
                                                                                                                                              TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
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APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
REGISTARTION NUMBER: 29,768
REFERENCE, DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                   Local
                                                                                                              STRANDEDNESS
                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                TOPOLOGY:
 37; Conservative
                   h 14.4%; Score 125; DB 16;
Similarity 25.2%; Pred. No. 2.4e-05;
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Pred. No. 2.4e-05;
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                                     DB 16;
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US-09-489-850-20
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                                                                                                                                                                  Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                        Best
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
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75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                       46 FSPRISAGYRINDLRFAVDYTRYKNY----
                                                                               15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS 74
                                                                                                                                                                                      Local
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                                                                                                                      6 AALIALALPAAALAEGASGFYVQADAAH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/988,444
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-193
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VAN ALSTYNE, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
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                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                37;
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/489,850 FILING DATE: 24-Jan-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                       LENGTH: 170 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP:
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                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 51916/103/INBI
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BENT, Stephen A.
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                                                                                                                                                                                      14.4%;
                                                                                                                                                                                                                                                                       SEQ ID NO: 20:
                                                                                                                                                                  18;
                                                                                                                                                                                      Score 125; DB 18;
Pred. No. 2.4e-05;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                         DB 18;
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                                                                                                                                                                    46;
                                                                                                                             ---AKASSSLGS-----AKG 45
                                           -----KAPSTDFK 79
                                                                                                                                                                                                            Length 170;
                                                                                                                                                                    Indels
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; ORGANISM: Agrobacterium tumefaciens US-09-803-110-11638
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT EPILCATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 11638
    Query Match
                                                                                                                                       SEQ ID NO 11638
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                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2000-02-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/168,139
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 13351
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)D
                                                                                                               LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 KLRNTSCSVNGLGCDPTTEHGGKGKWRFAYALMAGASIDVTCNLKADIGYRFRHINKGDM 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 SFSKTSA---GLG---------VLAGVSYAVTPNVDLDAGYRYNYVGKVNT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CGSVPGRCVSADLSSLSAYTLMANAYYDLGTYGSITPYVG-------GGIGGSYVKWD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 FAYENGGGPGRDKGLYSHEVRVGGRYVF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 V-----KNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 ASSLGLSATYDFKLKGKFKPYTGARVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GAHYYQGGPGGYLQDFDTATIKDSYVIGGGVGYQFNNYFRSDVTLDYMGKSDFRGSTSGF 120
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    14.3%;
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  Score 124.5;
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Pred. No. 5.6e-05;
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  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
  22;
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Length 281;
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US-09-540-236-2245

(Sequence 2245, Application US/09540236

(SERERAL INFORMATION:

(APPLICANT: Gary L. Breton et al.

(APPLICANT: Gary L. Breton et al.

(TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CA.

(TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

(FILE REFERENCE: 2709-2005-00]
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TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13699
                                                                                                                                                                                       RESULT 12
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NUMBER OF SEQ ID NOS:
SEQ ID NO 13699
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                                        166 GKDGNRDNTLADGAYAGVNFRF 187
                                                                                                                                                                                                                                                                                                                                                                                     100 YFGARLSLNRASAHLGGSDSFSKTSAGLGV-----LAGVSYAVTPNVDLDAGYRY-NYV 152
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                                                                                                                                                                                                                                                                                                     GKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                            GGGAELPLGQYFT-LFGEGYYSPDSMSSGVEDYVEANAGVRLNVRPSLNIEAGYRYIDMA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                          DGDSVGLGMGYNFNLGPF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKSIAAKMVAVTIALGASSAACAAVNLHGEAGAEFTNLSASFGAGEPGMTFSSQWAHSDN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKKALAALIA--LALPAAALAEGASGFYYQADAAHAKASSSLGSAK----- 44
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US/09/540,236
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29; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                   -LMTLGGKAVYLNPKDGDEGYAIAA 106
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RESULT 13
US-09-252-691-9162; Sequence 9162; Ap
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US-09-540-236-2245
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US-09-252-691C-9162
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NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Keith G
                                CURRENT APPLICATION NUMBER: US/09/252,691C CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/094,145 PRIOR FILING DATE: 1998-07-24 PRIOR APPLICATION NUMBER: US 60/074,787 PRIOR FILING DATE: 1998-02-18 NUMBER OF SEQ ID NOS: 11326 SEQ ID NO 9162
                                                                                                                                                                                                                                                                                        Sequence 9162, Application US/09252691C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 9162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
                                                                                                                                                                                                      APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 217
TYPE: PRT
                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 RPYIGAGVNYTTFFDEKFNDTGKEAGLSDLSLKDSWGMAGQVGLDYLINRDWLINASVWY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 VDLDAGYRYNYVGK---VNTVKNVRSGELSAGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 ETKVGFGVLAGAQYAINPQLSVDAGVEYNYLGKYDKLDTASKLKAHQYGAKVGLRHNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TQLGLTFTYMATDNVGVELLAATPFRHRVGLGPTGDIATVHHLPPTLMAQWYFGDSSSKV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LRFAVDYT----YDFDTQSPV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 12.3%; Score 107; DB 16
Local Similarity 22.9%; Pred. No. 0.0037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 MKKLAVAALILSSLSGGAYAHEAGEFFIRAGSATVRPTEGSDNVLGM-----GGFNVSNN 62
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                                                                                                                                                                                                                                               US-08-065-442-2
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (216) 241-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
ETILING DATE: 19930518
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLIACK, MATY E.
REGISTRATION NUMBER: 34,82
                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
TOPOLOGY: line
MOLError
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
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  60
                                                                                                                                                                                  Local Similarity
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                                          54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPV----KP----YFGAR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                1 MKKTAIALVVAGLAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
                                                                                                                      1 MKKALAALIALALPAAALAEGA---SGFYVQADAA----HAKASSSLGSAKGFSPRISAG 53
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YRRNTFTYGV----FGGYQILNQD--NFGLAAELGYDDFGRAKLREAGKPKAKHTNHGAY 113
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44114-2688
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                                                                                                                                                                                                                                                                                                                                                                                                              (216) 622-8458
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                                                                                                                                                                               12.0%; Score 104; DB 4
24.7%; Pred. No. 0.017;
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                                                                                                                                                                                                     DB_4; Length 359;
                                                                                                                                                                   82;
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Sear Job	рb	Qy	рb	Qy
ch com	174	137	114	105
Search completed: October 28, 2002, 16:11:24 Job time : 104.601 secs	174 VLPELAVRLEYQWLTRVGKYRPQDKPNTAINYNPWIGCINAGISYRF 220	137 VTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174	114 LSLKGSYEVLDGLDVYGKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYA 173	105 LSLNRASAHLGGSDSFSKTSAGL

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Minimum DB seq length: 0
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Sequence 4, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 153, App
Sequence 151, App
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Sequence 9349, Appli
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Sequence 8, Appli
Sequence 80, Appli
Sequence 760, App
Sequence 67258, Ap
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Sequence 14, Appl	Sequence 388, App	Sequence 5, Appli	Sequence 15330, A	Sequence 19380, A	Sequence 16088, A	Sequence 15697, A		193	80	Sequence 4, Appli	Sequence 45589, A		Sequence 45591, A	57139,	Sequence 57141, A	Sequence 98389, A	Sequence 23, Appl	Sequence 59699, A	Sequence 45753, A		Sequence 970, App	Sequence 17890, A		Sequence 7041, Ap

ALIGNMENTS

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RESULT 1
US-09-684-883-8
; Sequence 8, Application US/09684883
; GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard
Martin, Denis
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington
                                                                                                                               NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 04
                                                                TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: USA
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Rioux, Clement
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-684-883-6
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US-09-684-883-6
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GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 174;
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                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                        NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                   TYPE: amino acid
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                                                                                                       LENGTH: 174 amino acids
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Rioux, Clement
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                                         Matches 164;
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Best Local Similarity
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                                                                                                                                                                                                                                                                         TELEFAX: (202)672-5
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-Oct-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/684,883
                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                         Conservative
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                   (202)672-5399
                                                           94.8%;
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                                                           Score 825; DB 9; Length 174; Pred. No. 6.9e-77;
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                                       Mismatches
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Best Local :
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                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATE: 06-0ct-2000
PRIOR APPLICATION UNMBER: US/08/913,362
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
APPLICATION THOPMARTION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
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61 FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSINRASAHLGGSDS 119
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                                                                                                                                                            Match 94.78;
Local Similarity 94.98;
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                                                                                             1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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Martin, Denis
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                                                        TYPE: amino acid
STRANDEDNESS: <U
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                                                                                                                                            Conservative
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Rioux, Clement
                                                                                                                                                                                                                                                                                                 <Unknown>
                                                                                                                                                        Score 823.5; DB 9
Pred. No. 9.9e-77;
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                                                                                                                                                                        DB 9;
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Best Local Similarity
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                                                                                                                                                                                                                                                Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
121
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                                                                                                        61 FAVDYTRYKNYK-APSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSINRASAHLGGSDS 119
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                                                                                                                                                            1 MKKALAALIALALPAAALAEGASGFYYQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM_PC compatible
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 2'
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ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brodeur, Bernard R
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                                                                                 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
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                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 175 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/684,883
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Rioux, Clement
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93.7%;
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US-09-684-883-26
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                                                                                                                       Sequence 9, Application US/10203942 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DENOEL, PHILIPPE
APPLICANT: POOLMAN, JAN
APPLICANT: THONNARD, JOELLE
TITLE OF INVENTION: HAEMODHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                       61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION NUMBER: US/08/913,362
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
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                                                                                                                                                                                                                                                                                                                                Conservative
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Rioux, Clement
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                                                                                                                                                                                                                                                                                                                                                      Score 133;
Pred. No.
                                                                                                                                                                                                                                                                                                                                Mismatches
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US-09-545-199F-153
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SEQ ID NO 153
LENGTH: 369
TYPE: PRT
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CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kennedy J., Michael TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions FILE REFERENCE: 28341/6227.NCP
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NUMBER OF SEQ ID NOS: 165
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NUMBER OF SEQ ID NOS: 9
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CURRENT FILING DATE: 2002-08-15
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TYPE: PRT
ORGANISM: Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DYYGKAGVALVRSDYKLYNENSSTLKKLGEHHRARASGLFAVGAEYAVLPELAVRLEYQW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 KPYFGARLSLNRASAHLGGSDSFSKTSAG------LGVLA-GVSYAVTPNVDLDAGY-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YGYFGGYQILNQNNLGLAVELGYDDFGRAKGREKGKTVVKHTNHGTHLSLKGSYEVLEGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 PRISAGYRI---NDLRFAV-----DYTRYKNYKAPSTDFKLYSIGA--SVIYDFDTQSPV 97
86 ---SVIYDFDTQSPV------KPYFGARLSLNRASAHLGGSDSFSKTSAGLGVLAGV 133
                                                59 YGINRNSVTYGVFGGYQILNQNNFGLAAELGYDYYGRVRGNVDEFRTVKHSAHGLNLALK 118
                                                                                           50 -----ISAGYRI---NDLRFAVD--YTRYKNYKAPSTDFKLYSIGA-----
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                                                                                                                                           1 MKKSLVALAVLS--AAAVAQAAPQQNTFYAGAKVGQSSFHHGVNQLKSGHDDRYNDKTRK 58
                                                                                                                                                                                        1 MKKALAALIALALPAAALAEGA---SGFYVQADAAHAKASSSLGSAK-GFSPR-----
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                                                                                                                                                                                                                                        1 Similarity 57; Conserv
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                                                                                                                                                                                                                                        ; Score 95; DB 9; ; Pred. No. 0.26; 27; Mismatches
                                                                                                                                                                                                                                           78; Indels
                                                                                                                                                                                                                                                                                      Length 369;
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US-09-990-004A-149
; Sequence 149, Application US/09990004A
; GENERAL INFORMATION:
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                                                                       ; ORGANISM: Eucalyptus grandis US-09-990-004A-149
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SEQ ID NO 151
LENGTH: 364
TYPE: PRT
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Best Local :
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Best Local Similarity
                        Query Match
                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/990,004A CURRENT FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US 09/327,373
                                                                                                                                                                                                                                                                                                                               APPLICANT: Lasham, Annette TITLE OF INVENTION: Methods for Modulating Celluar Development and Programmed Cell DeFILE REFERENCE: 11000.1038c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/545,199F CURRENT FILING DATE: 2000-04-06 PRIOR APPLICATION NUMBER: 60/153,453 PRIOR FILING DATE: 1999-09-10 PRIOR APPLICATION NUMBER: 60/128,689 PRIOR APPLICATION NUMBER: 60/128,689 PRIOR FILING DATE: 1999-04-09 PRIOR FILING DATE: 1999-04-09 PRIOR FILING DATE: 1999-04-09
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                                                                                                                                                                                                             PRIOR FILING DATE: 199
NUMBER OF SEQ ID NOS:
                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 LKPSYEVLPDLDVYGKV----GIAL-VNNTYKTFNAAQEKVKTRRFQSSLILGAGVEYAI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYAILP---ELAARVEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRF 224
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10.3%;
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Score 90;
Pred. No.
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DB 9;
1.3;
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RESULT 12
US-09-791-537-117254
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US-10-219-220-149
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; ORGANISM: Moraxella catarrhalis US-09-791-537-117254
                                     APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: DOI-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 117254
LENGTH: 576
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Best Local
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-08-14 PRIOR APPLICATION NUMBER: U.S. NO. PRIOR FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 DRSGRRLGRARS------DRYAVAAGEELPASVDWRKEGAVVDVKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 NRASAHLGGSDSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 DRSGRRLGRARS------DRYAVAAGEELPASVDWRKEGAVVDVKD 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYNALGEKEKRFQVFKDNLRFIDDHNAGGD-RTYTVGLNQFADLTNEEYRSMYLGAR--M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NDLRFAY--DYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAVAVLALALITTIASALDMSIVSYDRAHGDRSSSSSSSWRSDDEVMAVYESWLAKHGK 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAVAVLALALTTIASALDMSIVSYDRAHGDRSSSSSSSWRSDDEVMAVYESWLAKHGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NDLRFAV--DYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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US-09-684-883-15
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US-09-684-883-15
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                   Query Match
Best Local Similarity
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 SAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 --DTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSVGKFN---ATAALGGYGSKSAV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 AIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIGVNYEF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 ASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDGRVTALDTKVNAL------ 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AEGASGFYVQADA-----AHAKASSSLGS-AKGFSPRISA-GYRINDLRFAVDYTR 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/684,883 FILING DATE: 06-Oct-2000 PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKNYKAPSTDFKLYSIGASVIYDFDTQSPV----KPYFGARLSLNRASAHLGGSDSFSKT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
    16;
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                                                                                                                             STRAIN: 608B
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
                                                                                                                                               ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rioux, Clement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamel, Josee
                                                                                                                                                                                                                                                                                                                 904136
10.0%; Score 87; DB 9; 100.0%; Pred. No. 0.032; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Score 87.5; DI 25.1%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Mismatches
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                                         Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 576;
Indels
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Gaps
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: MITHOES DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY I
TITLE OF INVENTION: MITHOUS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOPTWARE: Patentin version 3.0
SEQ ID NO 112202
LENGTH: 213
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 9349
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                Sequence 9349, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 112202, App. GENERAL INFORMATION:
                                                                                     Matches 44;
                                                                                                                          Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/540,209B CURRENT FILING DATE: 2000-04-04
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                                                                                                                                                                                         ORGANISM: B.fragilis
                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 DSFSKTSAGLGVLAGVSYAVTPNVDLDAGYRY-----NYVGKVNTVKN-VRSGELSAGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 PAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISA----GYRINDLRFAVDYTRYK 69
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 NYKAPSTD-----FKLYSIGASVIYDFDTQSPVKPYF----GARLSLNRASAHLGGS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 PQYSWAGGYTGLYLGYGWNKAK-TSTVGSIKPDDWKAGAFAGWNFQKDQIVYGVEGDAGY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FAVDYTRYKNYKAPST 76
32 MKKYTLYALYALALSSCNSDPKFNYKGDVSGADGKMLYLEASGLEGIVPLDSIKLKGDGS 91
                                         1 MKK-ALAALIALAAA-----ALAEGASG--FYVQA------DAAHAKASSS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FAVDYTRYKNYKAPST 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWAKKSKDGLEVKQGFE-GSLRARVGYDL---NPVMPYLTAGIAGSQIKLN-----NGL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                     Conservative
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                                                                                                      9.8%;
27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 87; DB 26.1%; Pred. No. 0.87 tive 30; Mismatches
                                                                                20; Mismatches 57; Indels
                                                                                                  Score 85; DB 9
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
0.87;
                                                                                                                          DB 9; Length 250;
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40 LGSAKGFSPRISAGYRI----NDLRFAVDYTRYKNYKAPSTDFK-LYSIGASVIYDFDTQ

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95 SPVKPYFGARLSLNR------ASAHLGGSDSFSKTSAGL 127

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146 AKIKELTIKQVRLQKDVDALVKAAQAHQLGNDVFEDSLAVL 186
                                                                           92 F-SFKQLRPESPEFYRLRVEDKVINFSVDSTETVSIQAPYTDFSTAYTVEGS-----ENS 145
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Search completed: October 28, 2002, 16:13:53 Job time: 36.6987 secs

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